

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2005, 09:45:35 ; Search time 39 Seconds
(without alignments)
86.348 Million cell updates/sec

Title: US-10-792-311-1

Perfect score: 166

Sequence: 1 AKKYAKKEKAKYKKEAKAKAEAAKAEAYEA 35

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 7756

Minimum DB seq length: 0

Maximum DB seq length: 35

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	26.5	33	2 A61310	nonhistone chromos
2	41.5	25.0	32	2 A41270	protamine S4 - sma
3	40	24.1	18	2 A61220	epsilon receptor m
4	39	23.5	25	2 S51071	ribosomal protein
5	39	23.5	33	2 A05162	antifreeze protein
6	38	22.9	33	1 F0F15G	antifreeze protein
7	36	21.7	33	2 T43163	metalloproteinase
8	35.5	21.4	30	2 B45316	sperm-specific pro
9	35	21.1	30	2 S02571	neurofilament trip
10	35	21.1	30	2 H95021	hypothetical prote
11	35	21.1	34	2 B97032	transcription regu
12	34.5	20.8	30	2 P00014	CAMP response elem
13	34	20.5	20	2 I53671	neurofilament heav
14	34	20.5	23	2 B04348	internal peptide v
15	34	20.5	30	2 E64577	hypothetical prote
16	34	20.5	35	2 A39525	histone H3 - mouse
17	34	20.5	35	2 A50612	hypothetical prote
18	33.5	20.2	35	2 A05112	M24 protein - Stre
19	33	19.9	22	2 D47256	kinetoplast DNA-as
20	33	19.9	24	2 A56753	lysine-rich 18K pr
21	33	19.9	27	2 A43768	Hu-like protein HB
22	33	19.9	29	2 T44245	ribosomal protein
23	33	19.9	32	2 A27074	histone H2A.2 - ra
24	32	19.3	20	2 S06149	photosystem I chai
25	32	19.3	20	2 S11416	ribosomal protein
26	32	19.3	29	2 AC0717	hypothetical prote
27	32	19.3	30	2 A49955	protein-tyrosine k
28	32	19.3	30	2 B81346	hypothetical prote
29	32	19.3	31	2 E70202	hypothetical prote

30 31.5 19.0 24 2 A48366 cytochrome c552 -
31 31.5 19.0 32 2 B40186 ubiquitin / riboso
32 31 18.7 20 2 S00315 photosystem I chai
33 31 18.7 20 2 B33290 histone H2B - huma
34 31 18.7 25 2 P00683 photosystem I 16.1
35 31 18.7 26 2 F49164 chromogranin-B - r
36 31 18.7 27 2 I54247 GTP-binding regula
37 31 18.7 29 2 S78412 ribosomal protein
38 31 18.7 33 2 S41226 transforming prote
39 31 18.7 33 2 PC2302 gaegurin 3 - Korea
40 30.5 18.4 34 2 S51069 ribosomal protein
41 30 18.1 11 2 P00682 photosystem I 17.5
42 30 18.1 15 2 P00692 photosystem I 18.5
43 30 18.1 16 2 A28144 ribosomal protein
44 30 18.1 16 2 B60278 24K antigen - Myco
45 30 18.1 23 2 A04348 internal peptide v

ALIGNMENTS

RESULT 1

A61310

nonhistone chromosomal protein HMG-14 - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 09-Jul-2004

C:Accession: A61310

R:Walker, J.M.; Goodwin, G.H.; Johns, E.W.

Int. J. Pept. Protein Res. 11, 301-304, 1978

A:Title: The amino terminal sequence of high mobility group non-histone chromosomal prote

A:Reference number: A61310; MUID:78217501; PMID:669887

A:Accession: A61310

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-33 <WAL>

A:Cross-references: UNIPROT:Q7M2Y3

C:Superfamily: nonhistone chromosomal protein HMG-17

C:Keywords: chromosomal protein

Query Match 26.5%; Score 44; DB 2; Length 33;
Best Local Similarity 38.5%; Pred. No. 1.7e+02;
Matches 10; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

OY 6 KKEAKKAYKKEAKAKAEAAKKA 31

DB 3 RKVSSAEGAKKEPKRRSARLSAKPA 28

RESULT 2

A41270

protamine S4 - smaller spotted catshark

N:Alternate names: scylliorhinine S4

C:Species: Scylliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)

C>Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 09-Jul-2004

C:Accession: A41270; S12285

R:Sautiere, P.; Guesse, M.; Briand, G.; Martinage, A.; Chevaillier, P.

Biochim. Biophys. Acta 791, 82-86, 1984

A:Title: Primary structure of scylliorhinine S4, a protamine isolated from sperm nuclei

A:Reference number: A41270

A:Accession: A41270

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-32 <SAU>

A:Cross-references: UNIPROT:P30259

R:Gusse, M.; Sautiere, P.; Chauviere, M.; Chevaillier, P.

Biochim. Biophys. Acta 748, 93-98, 1983

A:Title: Extraction, purification and characterization of the sperm protamines of the dog

A:Reference number: S01463; MUID:84000513; PMID:6615852

A:Accession: S12285

A:Molecule type: protein

A:Residues: 1-5 <GUS>

C:Keywords: DNA binding; sperm; testis

Query Match 25.0%; Score 41.5; DB 2; Length 32;
Best Local Similarity 37.9%; Pred. No. 3e+02;
Matches 11; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

QY 2 KKAYKKEKAACKVKKKEAKAARAAAKE 30
DB 4 KRVARKPKCKKA-RKRPCKRRRKVAKK 31

RESULT 3
A61220
epsilon receptor modulating protein (EC 3.4.21.-) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: A61220
R;Matushita, S.; Katz, D.H.
Cell Immunol. 137, 252-259, 1991
A;Title: The murine epsilon receptor modulating protein: a novel serine protease which m
A;Reference number: A61220; PMID:91356570; PMID:1679381
A;Accession: A61220
A;Molecule type: protein
A;Residues: 1-18 <MAT>
A;Cross-references: UNIPROT:Q7M060
C;Comment: This serine proteinase from a T cell hybridoma does not reduce levels of CD23
C;Keywords: hydrolase; serine proteinase

Query Match 24.1%; Score 40; DB 2; Length 18;
Best Local Similarity 60.0%; Pred. No. 2.7e+02;
Matches 12; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 11 AKKAYKKEAKAARAAAKE 30
DB 1 AKPAPKKEKK-KAAAKK 18

RESULT 4
S51071
ribosomal protein S20 - Thermus aquaticus (fragment)
C;Species: Thermus aquaticus
C;Date: 15-Jul-1995 #sequence_revision 01-Nov-1996 #text_change 01-Nov-1996
C;Accession: S51071
R;Tsiboli, P.; Herfurth, E.; Choli, T.
Eur. J. Biochem. 226, 169-177, 1994
A;Title: Purification and characterization of the 30S ribosomal proteins from the bacter
A;Reference number: S51053; PMID:95045586; PMID:7957245
A;Accession: S51071
A;Molecule type: protein
A;Residues: 1-25 <TSI>
A;Note: the source is designated as Thermus thermophilus
C;Keywords: protein biosynthesis; ribosome

Query Match 23.5%; Score 39; DB 2; Length 25;
Best Local Similarity 42.9%; Pred. No. 4.5e+02;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 3 KYAKKEKAACKVKKKEAKA 23
DB 3 KNAPKKEAGRRPTRKAKXA 23

RESULT 5
A05162
antifreeze protein SS-3 - shorthorn sculpin
C;Species: Myoxocephalus scorpius (shorthorn sculpin, daddy sculpin)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C;Accession: A05162
R;Hew, C.L.; Joshi, S.; Wang, N.C.; Kao, M.H.; Ananthanarayanan, V.S.
Eur. J. Biochem. 151, 167-172, 1985
A;Title: Structures of shorthorn sculpin antifreeze polypeptides.
A;Reference number: A91150; PMID:85285003; PMID:4029130
A;Accession: A05162
A;Molecule type: protein
A;Residues: 1-33 <HEW>

C;Species: *Mytilus californianus* (California mussel)
 C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C;Accession: B45316
 R;Carlos, S.; Jutglar, L.; Borrell, I.; Hunt, D.F.; Ausio, J.
 J. Biol. Chem. 268, 185-194, 1993
 A;Title: Sequence and characterization of a sperm-specific histone H1-like protein of *Mytilus californianus*
 A;Reference number: A45316; MUID:93106999; PMID:7677995
 A;Accession: B45316
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-35 <CAR>
 A;Cross-references: UNIPROT:P35422
 A;Note: sequence extracted from NCBI backbone (NCBIP:121400)
 C;Keywords: DNA binding

Query Match 21.7%; Score 36; DB 2; Length 35;
 Best Local Similarity 56.2%; Pred. No. 1.2e+03;
 Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 5 AKKEKAAYKKEAK 20
 Db 20 ASAGKAARAKSKTAK 35

RESULT 9
 S02571
 neurofilament triplet protein H - pig (fragment)
 C;Species: *Sus scrofa domestica* (domestic pig)
 C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 10-Dec-1999
 C;Accession: S02571
 R;Geisler, N.; Vandekerckhove, J.; Weber, K.
 FEBS Lett. 221, 403-407, 1987
 A;Title: Location and sequence characterization of the major phosphorylation sites of the neurofilament triplet protein H
 A;Reference number: S02570; MUID:87304852; PMID:3114005
 A;Accession: S02571
 A;Molecule type: protein
 A;Residues: 1-30 <GEI>
 A;Experimental source: spinal cord
 A;Note: 5-Glu, 19-Glu, and 21-Glu were also found
 C;Superfamily: neurofilament triplet H protein
 C;Keywords: coiled coil; heterotrimer; intermediate filament; nerve; phosphoprotein
 F;3.17/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 21.4%; Score 35.5; DB 2; Length 30;
 Best Local Similarity 44.8%; Pred. No. 1.2e+03;
 Matches 13; Conservative 3; Mismatches 6; Indels 7; Gaps 2;

Qy 11 AKKAYKKEA---KAKA---AEAAKAA 32
 Db 1 AKSPVKEAKSPKAKSPVKAASPEXA 29

RESULT 10
 H95021
 hypothetical protein SP0188 [imported] - *Streptococcus pneumoniae* (strain TIGR4)
 C;Species: *Streptococcus pneumoniae*
 C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
 C;Accession: H95021
 R;Tetelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
 on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapf
 le, T.; Hickey, E.K.; Holt, I.E.
 Science 293, 498-506, 2001
 A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
 A;Title: Complete Genome Sequence of a virulent isolate of *Streptococcus pneumoniae*.
 A;Reference number: A95000; MUID:21357209; PMID:11463916
 A;Accession: H95021
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-30 <KUR>
 A;Cross-references: UNIPROT:Q97SK5; GB:AE005672; PIDN:AAK74369.1; PID:gl4971656; GSPDB:G
 A;Experimental source: strain TIGR4
 C;Genetics:
 A;Gene: SP0188

Query Match 21.1%; Score 35; DB 2; Length 30;
 Best Local Similarity 58.3%; Pred. No. 1.4e+03;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 KKAYKKEAAKK 13
 Db 4 KKYENDEKSQKK 15

RESULT 11
 B97032
 transcription regulator, *ActR* family [imported] -- *Clostridium acetobutylicum*
 C;Species: *Clostridium acetobutylicum*
 C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
 C;Accession: B97032
 R;Nolling, J.; Breton, G.; Omeichenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
 J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4823-4838, 2001
 A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium *Clostridium acetobutylicum*
 A;Reference number: A96900; MUID:21359325; PMID:21359325
 A;Accession: B97032
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-34 <KUR>
 A;Cross-references: UNIPROT:Q97KS0; GB:AE001437; PIDN:AAK79045.1; PID:gl5023984; GSPDB:G
 A;Experimental source: *Clostridium acetobutylicum* ATCC824
 C;Genetics:
 A;Gene: CAC1071

Query Match 21.1%; Score 35; DB 2; Length 34;
 Best Local Similarity 31.8%; Pred. No. 1.5e+03;
 Matches 7; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy 2 KKAYKKEAAKKAYKKEAKAKA 23
 Db 4 RRFVKTETAIKAFITLLKES 25

RESULT 12
 PD0014
 CAMP response element-binding protein 11.2K, 16K - rat (fragment)
 C;Species: *Rattus norvegicus* (Norway rat)
 C;Date: 10-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004
 C;Accession: PD0014
 R;Lee, M.Y.; Hwang, E.S.; Lee, S.K.
 Biochem. Biophys. Res. Commun. 246, 50-54, 1998
 A;Title: Novel CRE-binding proteins of 11-16 kDa bind to the LDH A-gene CRE in a sequence
 A;Reference number: PD0013; MUID:98262915; PMID:9600066
 A;Contents: Liver
 A;Accession: PD0014
 A;Molecule type: protein
 A;Residues: 1-30 <LEE>
 A;Cross-references: UNIPROT:Q7M0A0
 C;Superfamily: histone H2B

Query Match 20.8%; Score 34.5; DB 2; Length 30;
 Best Local Similarity 46.2%; Pred. No. 1.5e+03;
 Matches 12; Conservative 1; Mismatches 12; Indels 1; Gaps 1;

Qy 5 AKKEKAAYKKEAKAKAAEAAAKE 30
 Db 4 AKSAPAPKKGSKK-AVTKAQKDDGKE 28

RESULT 13
 I53671
 neurofilament heavy subunit - human (fragment)
 C;Species: *Homo sapiens* (man)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C;Accession: I53671
 R;Figlewicz, D.A.; Rouleau, G.A.; Krizus, A.; Julien, J.P.
 Gene 132, 297-300, 1993

Db 2 KFYSKNEVLQKRVFKQQ 18
Search completed: June 3, 2005, 10:00:32
Job time : 41 secs

A;Title: Polymorphism in the multi-phosphorylation domain of the human neurofilament head
A;Reference number: I53671; MUID:94040777; PMID:8224877
A;Accession: I53671
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-20 <RES>
A;Cross-references: UNIPROT:Q16070; GB:S66488; NID:9452861; PIDN:AA528609.1; PID:9452862
C;Genetics:
A;Gene: GDB:NRFH
A;Cross-references: GDB:I20225; OMIM:162230
A;Map position: 22q12.1-22q13.1

Query Match 20.5%; Score 34; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 5 AKKEAKAKYKKEAK 20
||| :||| :|||
Db 5 AKSPEAKAKSPEKEAK 20

RESULT 14
B04348
Internal peptide VII - phage T6
C;Species: phage T6
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: B04348; A04348
R;van Eerd, J.P.; Champe, S.P.; Yager, L.; Kubota, I.; Tsugita, A.
J. Mol. Biol. 117, 521-524, 1977
A;Title: Primary structure of internal peptide VII of T-even bacteriophages.
A;Reference number: A92849; MUID:78111436; PMID:604510
A;Accession: B04348
A;Molecule type: protein
A;Residues: 1-23 <VANS>
A;Cross-references: UNIPROT:P21597
C;Comment: This protein is a cleavage product of P22 protein that is incorporated into bacteriophage T4.
C;Superfamily: phage T4 gene 22 protein
C;Keywords: head protein

Query Match 20.5%; Score 34; DB 2; Length 23;
Best Local Similarity 57.1%; Pred. No. 1.4e+03;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 7 KEKAARAKYKKEAK 20
||| :||| :|||
Db 10 KEAEERAKKEKIAE 23

RESULT 15
E64577
Hypothetical protein HP0461 - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: E64577
R;Tomb, J.F.; White, O.; Kexlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.; Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: E64577
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-30 <TOM>
A;Cross-references: UNIPROT:Q25208; GB:AE000561; NID:G2313564; PIDN:AA00753

Query Match 20.5%; Score 34; DB 2; Length 30;
Best Local Similarity 35.3%; Pred. No. 1.7e+03;
Matches 6; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 2 KKYAKKEAKKAYKKE 18
||| :||| :|||

Result No.	Score	Query %		DB	ID	Description
		Match	Length			
1	67	40.4	35	2	Q747M3	Q747M3 geobacter s
2	46	27.7	22	2	Q77Q96	Q77Q96 psammechinu
3	45	27.1	33	1	DDSK_PHYDS	P83638 phyllomedus
4	44	26.5	33	2	Q7W2Y3	Q7W2Y3 sus scrofa
5	43	25.9	35	2	Q83175	Q83175 cauliflower
6	41.5	25.0	32	1	PR74 SCYA	P30259 scyliorhinu
7	41	24.7	32	2	Q8P382	Q8P382 xanthomonas
8	40	24.1	18	2	Q7M060	Q7M060 mus musculu
9	39	23.5	17	2	Q9TWR3	Q9TWR3 trypanosoma
10	39	23.5	32	1	CEC_OIKKI	P83420 oiketicus k
11	39	23.5	20	1	ANF3 MYOSC	P04367 myoxocephal
12	38	22.9	20	2	Q7TWH1	Q9TWH1 trypanosoma
13	38	22.9	33	1	ANP5 MYOAE	P20421 myoxocephal
14	38	22.9	35	1	CUID_CUPSA	P83622 cupiennius
15	38	22.9	35	2	Q7RCL9	Q7RCL9 plasmodium
16	37.5	22.6	29	1	RM40 RAT	P83565 rattus norv
17	37	22.3	35	1	CUIB_CUPSA	P83620 cupiennius
18	37	22.3	35	1	CUIC_CUPSA	P83621 cupiennius
19	36	21.7	19	2	P83197	P83197 oryza sativ
20	36	21.7	28	2	O81Q23	O81Q23 bacillus an
21	36	21.7	33	2	Q48578	Q48578 listeria iv
22	36	21.7	35	1	CUIA_CUPSA	P83619 cupiennius
23	36	21.7	35	1	PH11_MYTCA	P35422 mytilus cal
24	35	21.1	29	2	Q92ZR0	Q92ZR0 rattus norv
25	35	21.1	30	2	Q97SX5	Q97SX5 streptococc
26	35	21.1	34	2	Q12681	Q12681 saccharomyc
27	35	21.1	34	2	Q7R3Z2	Q7R3Z2 plasmodium
28	35	21.1	34	2	Q97K50	Q97K50 clostridium
29	35	21.1	35	2	Q71ZB8	Q71ZB8 listeria mo
30	34.5	20.8	30	2	Q7M0A0	Q7M0A0 rattus norv
31	34	20.5	20	2	Q16070	Q16070 homo sapien


```

RN SEQUENCE FROM N.A.
RP MEDLINE=79001915; PubMed=688387; DOI=10.1016/0092-8674(78)90249-0;
RA Schaffner W., Kunz G., Dactwyler H., Telford J., Smith H.O.,
RA Birnstiel M.L.;
RT "Genes and spacers of cloned sea urchin histone DNA analyzed by
RT sequencing.";
RL Cell 14:655-671(1978).
DR EMBL: J01184; AAB59209.1; -.
FT NON TER 1
SQ SEQUENCE 22 AA; 2244 MW; 56699BDE54970875 CRC64;

Query Match 27.7%; Score 46; DB 2; Length 22;
Best Local Similarity 57.1%; Pred. No. 3.4e+02;
Matches 12; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Oy 2 KYAKKEKAAYKKAAYKKAAYK 22
Db 2 KPAAKKPAKKPAKKPAKKVAKSK 22

RESULT 3
DDSK_PHYDS STANDARD; PRT; 33 AA.
ID P83638;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Dermadistinctin K (DD K).
OS Phyllomedusa distincta (Monkey frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;
OC Phyllomedusinae; Phyllomedusa.
OC NCBI_TaxID=164618;

RN SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, MASS
RP SPECTROMETRY, CIRCULAR DICHROISM ANALYSIS, AND SYNTHESIS.
RC TISSUE=Skin secretion;
RX MEDLINE=99404773; PubMed=10477123; DOI=10.1016/S0196-9781(99)00050-9;
RA Batista C.V.F., da Silva L.R., Sebben A., Scaloni A., Ferrara L.,
RA Paiva G.R., Olamendi-Portugal T., Possani L.D., Bloch C. Jr.;
RT "Antimicrobial peptides from the Brazilian frog Phyllomedusa
RT distincta.";
RL Peptides 20:679-686(1999).

RN SEQUENCE, AND ANTIPROTOZOAL ACTIVITY.
RP MEDLINE=22370988; PubMed=12379643; DOI=10.1074/jbc.M209289200;
RA Brand G.D., Leite J.R.S.A., Silva L.P., Albuquerque S., Prates M.V.,
RA Azevedo R.B., Carregaro V., Silva J.S., Sa V.C.L., Brandao R.A.,
RA Bloch C. Jr.;
RT "Dermaseptins from Phyllomedusa oreades and Phyllomedusa distincta.
RT Anti-trypanosoma cruzi activity without cytotoxicity to mammalian
RT cells.";
RL J. Biol. Chem. 277:49332-49340(2002).

CC -1- FUNCTION: Antibacterial activity against Gram-positive bacterium
CC S. aureus and E. faecalis, and Gram-negative bacterium P. aeruginosa
CC and E. coli. Has antiprotzoal activity against T. cruzi.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- MASS SPECTROMETRY: MW=3154.0; METHOD=Electrospray; RANGE=1-33;
CC NOTE=Ref.1.
CC -1- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
CC Dermaseptin subfamily.
KW Amphibian defense peptide; Antibiotic; Direct protein sequencing.
SQ SEQUENCE 33 AA; 3153 MW; 2A6A282029A47547 CRC64;

Query Match 27.1%; Score 45; DB 1; Length 33;
Best Local Similarity 46.9%; Pred. No. 6.2e+02;
Matches 15; Conservative 4; Mismatches 11; Indels 2; Gaps 1;

Oy 4 YAKKEKAAYKKAAYKKAAYKKAAYK 35
Db 3 WSKAKAGKEAAK-AAAKAGKAALNAVSEA 32

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RESULT 4
Q7M2Y3 PRELIMINARY; PRT; 33 AA.
ID Q7M2Y3
AC Q7M2Y3; 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nonhistone chromosomal protein HMG-14 (Fragment).
OS Sus scrofa domestica (domestic pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC NCBI_TaxID=9825;
RN NCBI_TaxID=9825;
RN [1]
RP SEQUENCE
RX MEDLINE=78217501; PubMed=669887;
RA Walker J.M., Goodwin G.H., Johns E.W.;
RT "The amino terminal sequence of high mobility group non-histone
RT chromosomal protein HMG 14, showing sequence homologies with two other
RT chromosomal proteins.";
RL Int. J. Pept. Protein Res. 11:301-304(1978).
DR PIR; A61310; A61310.
DR GO; GO:0000785; C:chromatin; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR000079; HMG14_17.
DR Pfam; PF01101; HMG14_17_1.
DR PRINTS; PR00925; NONHISHMG17.
DR PROSITE; PS00355; HMG14_17; 1.
DR FT NON TER 1
DR FT NON TER 33
SQ SEQUENCE 33 AA; 3531 MW; 9EC7492EA8CAEA2B CRC64;

Query Match 26.5%; Score 44; DB 2; Length 33;
Best Local Similarity 38.5%; Pred. No. 7.9e+02;
Matches 10; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Oy 6 KKEKAAYKKAAYKKAAYKKAAYK 31
Db 3 RKVSSAAGAAKEPKRRSARLSAKPA 28

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RESULT 5
Q83175 PRELIMINARY; PRT; 35 AA.
AC Q83175;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Coat protein, partial cds. (Fragment).
OS Cauliflower mosaic virus.
OC Viruses; Retroid viruses; Caulimoviridae; Caulimovirus.
OC NCBI_TaxID=10641;
RN NCBI_TaxID=10641;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90320145; PubMed=2371775;
RA Vaden V.R., Melcher U.K.;
RT "Recombination sites in cauliflower mosaic virus DNAs: implications
RT for mechanisms of recombination.";
RL Virology 177:717-726(1990).
DR EMBL; M32814; AAA46352.1; -.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
KW Coat protein.
FT NON TER 1
FT NON TER 35
SQ SEQUENCE 35 AA; 4552 MW; 472F3CE98D4C46A6 CRC64;

Query Match 25.9%; Score 43; DB 2; Length 35;
Best Local Similarity 47.6%; Pred. No. 1.1e+03;
Matches 10; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

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QY 2 KKYAKKEAAKAYKKEAKAK 22
 DB 7 KKYHKRYKKYKVKYPYKKKK 27

RESULT 6

RA SCYCA STANDARD; PRT; 32 AA.
 AC P30259;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Protamine S4.
 OS Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
 OC Scyllorhinidae; Scyllorhinus.
 OX NCBI_TaxID=7830;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Testis;
 RA Sautiere P., Gusse M., Briand G., Martinge A., Chevaillier P.;
 RT "Primary structure of scyllorhinine S4, a protamine isolated from
 sperm nuclei of the dog-fish Scyllorhinus caniculus";
 RL Biochim. Biophys. Acta 791:82-86(1984).
 CC -!- FUNCTION: Protamines substitute for histones in the chromatin of
 sperm during the haploid phase of spermatogenesis. They compact
 sperm DNA into a highly condensed, stable and inactive complex.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- TISSUE SPECIFICITY: Testis.
 DR PIR; A41270; A41270.
 KW Chromosomal protein; Direct protein sequencing; DNA condensation;
 KW DNA-binding; Nuclear protein; Nucleosome core; Spermatogenesis;
 KW Testis.
 SQ SEQUENCE 32 AA; 3882 MW; 4C4E9F58958D1AEF CRC64;

Query Match 25.0%; Score 41.5; DB 1; Length 32;
 Best Local Similarity 37.9%; Pred. No. 1.4e+03;
 Matches 11; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

QY 2 KKYAKKEAAKAYKKEAKAK 30
 DB 4 KKKAKRPCKKA-RKPCKRKVKKK 31

RESULT 7

RA SCYCA PRELIMINARY; PRT; 32 AA.
 AC Q8P382;
 DT 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
 DE Hypothetical protein XCC4196.
 GN OrderedLocustNames=XCC4196;
 OS Xanthomonas campestris (pv. campestris).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xanthomonas.
 OX NCBI_TaxID=340;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 33913 / NCPPB 528;
 RX MEDLINE=2022145; PubMed=12024217; DOI=10.1038/417459a;
 RA da Silva A.C.R., Ferro J.A., Reinach P.C., Farah C.S., Furlan L.R.,
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
 RA Camarotte G., Cannavan F., Cardoso J., Chambergo F., Ciapina L.P.,
 RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
 RA Faria J.B., Ferreira A.J.C., Ferreira R.C.C., Ferro M.I.T.,
 RA Fornighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
 RA Katayama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
 RA Locati E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
 RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
 RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
 RA Trindade dos Santos M., Truffi D., Teai S.M., White F.F.,
 RA Setubal J.C., Kitajima J.P.;
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing
 host specificities";
 RL Nature 417:459-463(2002).
 DR EMBL; AE012546; AAM43412.1; -.
 KW Complete proteome.
 SQ SEQUENCE 32 AA; 3674 MW; 72C4849D4149F3EA CRC64;

Query Match 24.7%; Score 41; DB 2; Length 32;
 Best Local Similarity 48.0%; Pred. No. 1.6e+03;
 Matches 12; Conservative 2; Mismatches 7; Indels 4; Gaps 1;

QY 2 KKYAKKEXA----AKKAYKKEAKAK 22
 DB 8 KKSQKKEPAKTLKEKRAAKQEKKGK 32

RESULT 8

QY7M060 PRELIMINARY; PRT; 18 AA.
 AC Q7M060;
 DT 01-MAR-2004 (TRENBLrel. 26, Created)
 DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Epsilon receptor modulating protein (EC 3.4.21.-) (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91356570; PubMed=1679381;
 RA Matsushita S., Katz D.H.;
 RT "The murine epsilon receptor modulating protein: a novel serine
 protease which modulates CD23 binding of IgE";
 RL Cell. Immunol. 137:252-259(1991).
 DR PIR; A61220; A61220.
 FT NON_TER 1
 FT NON_TER 18
 FT NON_TER 18
 SQ SEQUENCE 18 AA; 1979 MW; 2DDC6EE422317373 CRC64;

Query Match 24.1%; Score 40; DB 2; Length 18;
 Best Local Similarity 60.0%; Pred. No. 1.2e+03;
 Matches 12; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 11 AKKAYKKEAKAKAAEAAKE 30
 DB 1 AKPAPKKEKKK--KAAAKK 18

RESULT 9

QY7WR3 PRELIMINARY; PRT; 17 AA.
 AC Q9TWR3;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
 DE Histone H1 (Fragment).
 OS Trypanosoma cruzi.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 OX NCBI_TaxID=5693;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94043510; PubMed=8227175;
 RA Toro G.C., Galanti N., Hellman U., Wernstedt C.;
 RT "Unambiguous identification of histone H1 in Trypanosoma cruzi";
 RL J. Cell. Biochem. 52:431-439(1993).
 SQ SEQUENCE 17 AA; 1820 MW; AD19BC52D8ECCD5 CRC64;

Query Match 23.5%; Score 39; DB 2; Length 17;

Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 8 EKAKEAKAYKKEAKAK 22
Db 3 KKAAPKAVKAPKKK 17

RESULT 10
CEC_OIKKI
ID CEC_OIKKI STANDARD; PRT; 32 AA.
AC P83420;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cecropin (Fragment).
OS Oiketicus kirbyi (Bagworm moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Tineoidea;
OC Psychidae; Oiketicinae; Oiketicus.
OX NCBI_TaxID=201386;
RN [1]

SEQUENCE, FUNCTION, SUBUNIT, SUBCELLULAR LOCATION, TISSUE SPECIFICITY,
AND MASS SPECTROMETRY.
TISSUE=Hemolymph;
RA Bulet P.;
RL Submitted (JUL-2002) to Swiss-Prot.
CC -1- FUNCTION: Cecropins have lytic and antibacterial activity against
CC several Gram-positive and Gram-negative bacteria. Has also
CC activity against fungi.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Hemolymph.
CC -1- MASS SPECTROMETRY: MW=3818.89; METHOD=VALDI; RANGE=1-?;
CC NOTE=Ref.1.

CC -1- SIMILARITY: Belongs to the cecropin family.
DR InterPro; IPR000875; Cecropin.
DR Pfam; PF00272; Cecropin; 1.
DR PROSITE; PS00268; CECROPIN; 1.
KW Antibiotic; Direct protein sequencing; Fungicide; Hemolymph;
KW Insect immunity.
FT NON TER 32
SQ SEQUENCE 32 AA; 3434 MW; F6942D09A7BDC1F0 CRC64;

Query Match 23.5%; Score 39; DB 1; Length 32;
Best Local Similarity 36.7%; Pred. No. 2.6e+03;
Matches 11; Conservative 4; Mismatches 15; Indels 0; Gaps 0;

Qy 2 KKYAKKEAKAYKKEAKAKAEAAKEA 31
Db 2 KPFFKIEKAVRRVDGVAKAGPAVVVGQA 31

RESULT 11
ANP3_MYOSC
ID ANP3_MYOSC STANDARD; PRT; 33 AA.
AC P04357;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Antifreeze peptide SS-3.
OS Myoxocephalus scorpius (Shorthorn sculpin) (Daddy sculpin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Scorpaeniformes;
OC Cottoidae; Cottidae; Myoxocephalus.
OX NCBI_TaxID=8097;
RN [1]

SEQUENCE.
RX MEDLINE=85285003; PubMed=4029130;
RA Hew C.-L., Joshi S., Wang N.-C., Kao M.H., Ananthanarayanan V.S.;
RT "Structures of shorthorn sculpin antifreeze polypeptides.";
RL Eur. J. Biochem. 151:167-172(1985).

RP SEQUENCE.
RX MEDLINE=96223980; PubMed=8626748; DOI=10.1074/jbc.271.8.4106;
RA Gong Z., Ewart K.V., Hu Z., Fletcher G.L., Hew C.-L.;
RT "Skin antifreeze protein genes of the winter flounder, *Pleuronectes americanus*, encode distinct and active polypeptides without the secretory signal and prosequences.";
RL J. Biol. Chem. 271:4106-4112(1996).
CC -1- FUNCTION: Antifreeze proteins lower the blood freezing point.
CC -1- SIMILARITY: Belongs to the type-1 AFP family.
DR PIR; A05162; A05162.
KW Antifreeze protein; Direct protein sequencing; Repeat.
SQ SEQUENCE 33 AA; 2939 MW; 8B74CC4C06A1208A CRC64;

Query Match 23.5%; Score 39; DB 1; Length 33;
Best Local Similarity 50.0%; Pred. No. 2.6e+03;
Matches 15; Conservative 1; Mismatches 12; Indels 2; Gaps 1;

Qy 5 AKKEAKAYKKEAKAK--AAEAAAKEAA 32
Db 3 APAPAAAKTAADALAAAKTAADAAAAA 32

RESULT 12
Q9TWH1
ID Q9TWH1 PRELIMINARY; PRT; 20 AA.
AC Q9TWH1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Histone H1 (Fragment).
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]

RP SEQUENCE.
RX MEDLINE=95375686; PubMed=7647705; DOI=10.1016/0248-4900(96)89928-X;
RA Burri M., Schlimme W., Betschart B., Lindner H., Kamfer U.,
RA Schaller J., Hecker H.;
RT "Partial amino acid sequence and functional aspects of histone H1 proteins in *Trypanosoma brucei* brucei.";
RL Biol. Cell 83:23-31(1995).
SQ SEQUENCE 20 AA; 1985 MW; 2D37ED343CE23F93 CRC64;

Query Match 22.9%; Score 38; DB 2; Length 20;
Best Local Similarity 64.3%; Pred. No. 2.1e+03;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AKKYAKKEAKAKA 14
Db 1 AKKAAPKKTAKKA 14

RESULT 13
ANP5_MYOAE
ID ANP5_MYOAE STANDARD; PRT; 33 AA.
AC P20421;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Antifreeze peptide GS-5.
OS Myoxocephalus aeneus (Grubby sculpin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Scorpaeniformes;
OC Cottoidae; Cottidae; Myoxocephalus.
OX NCBI_TaxID=8096;
RN [1]

SEQUENCE.
RA Chakrabarty A., Hew C.-L., Shears M., Fletcher G.;
RT "Primary structures of the alanine-rich antifreeze polypeptides from grubby sculpin, *Myoxocephalus aeneus*.";
RL Can. J. Zool. 66:403-408(1988).


```

CC -!- FUNCTION: Antifreeze proteins lower the blood freezing point.
CC -!- SIMILARITY: Belongs to the type-I AFP family.
DR PIR; S06417; FDF15G.
KW Antifreeze protein; Direct protein sequencing; Repeat.
FT MOD RES 1 1 Blocked amino end (Met).
SQ SEQUENCE 33 AA; 2980 MW; 7F2ACC56B70A2080 CRC64;

Query Match 22.9%; Score 38; DB 1; Length 33;
Best Local Similarity 48.0%; Pred. No. 3.4e+03;
Matches 12; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 5 AKKEAKAAKAYKKEAKAKAAKAAK 29
DB 8 AAKTAADALAAAKTAADAAAK 32

RESULT 14
ID_CUID_CUPSA STANDARD; PRT; 35 AA.
AC P83622;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cupiennin 1d.
OS Cupiennius salei (Wandering spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Cupiennius.
OX NCBI_TaxID=6928;
RN [1]
RP SEQUENCE, SYNTHESIS, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
RC TISSUE=Venom;
RX MEDLINE=21909535; PubMed=11792701; DOI=10.1074/jbc.M11099200;
RA Kuhn-Nentwig L., Mueller J., Schaller J., Walz A., Dathe M.,
RA Nentwig W.;
RT "Cupiennin 1, a new family of highly basic antimicrobial peptides in
RT the venom of the spider Cupiennius salei (Ctenidae).";
RL J. Biol. Chem. 277:11208-11216(2002).
RN [2]
RP FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=20132510; PubMed=10669026; DOI=10.1016/S0041-0101(99)00167-1;
RA Hasberli S., Kuhn-Nentwig L., Schaller J., Nentwig W.;
RT "Characterisation of antibacterial activity of peptides isolated from
RT the venom of the spider Cupiennius salei (Araneae: Ctenidae).";
RL Toxicon 38:373-380(2000).
CC -!- FUNCTION: Has antimicrobial activity against B. subtilis, E.coli,
CC E.faecalis, P.aeruginosa, and S.aureus. Has insecticidal and
CC hemolytic activities. Probably acts by disturbing membrane
CC function with its amphipathic structure.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- MASS SPECTROMETRY: MW=3795.13; MW_ERR=0.79; METHOD=Electrospray;
CC RANGE=1-35; NOTE=Ref. 1.
CC -!- MASS SPECTROMETRY: MW=3794.89; METHOD=Electrospray; RANGE=1-35;
CC NOTE=Ref. 2.
KW Amidation; Antibiotic; Direct protein sequencing; Hemolysis;
KW Neurotoxin; Toxin.
FT MOD RES 35 35 Glutamic acid 1-amide.
SQ SEQUENCE 35 AA; 3797 MW; AE1677338BA73894 CRC64;

Query Match 22.9%; Score 38; DB 1; Length 35;
Best Local Similarity 50.0%; Pred. No. 3.5e+03;
Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 16 KKEAKAKAAEAKEAAYEA 35
DB 11 KKVAKTVAKQAAKQAGKYVA 30

RESULT 15
Q7RC19 PRELIMINARY; PRT; 35 AA.
ID Q7RC19
AC Q7RC19;

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DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE Hypothetical protein (Fragment).
GN Name=PV05965;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Aguioli S.V., Suh B.B., Kooij T.W., Perteau M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.B.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., O.R.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., M.J.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01001963; EAA18097.1; -.
KW Hypothetical protein.
FT NON_TER 35
SQ SEQUENCE 35 AA; 4472 MW; D9B2098F0710372A CRC64;

Query Match 22.9%; Score 38; DB 2; Length 35;
Best Local Similarity 58.3%; Pred. No. 3.5e+03;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 YAKKEKAACKAY 15
DB 4 YSKKKKKKKKKY 15

Search completed: June 3, 2005, 09:59:48
Job time : 173 secs

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OM protein - protein search, using sw model
Run on: June 3, 2005, 09:18:04 ; Search time 158 Seconds
(without alignments)
85.675 Million cell updates/sec

Title: US-10-792-311-1
Perfect score: 166
Sequence: 1 AKYAKKEKAAKAYKKEKAKAARAAKAEAYEA 35

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 854512

Minimum DB seq length: 0
Maximum DB seq length: 35

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	166	100.0	35	3	AA82571 Copolymer
2	71	42.8	31	8	ADN11701 Peptide 1
3	67.5	40.7	32	2	AA90180 Polycatio
4	67.5	40.7	32	2	AAW06686 Protamine
5	67.5	40.7	32	3	AA808168 Peptide m
6	67.5	40.7	33	2	AA90181 Polycatio
7	67.5	40.7	33	2	AAW06688 Protamine
8	65	39.2	25	7	ADJ81216 Self-asse
9	65	39.2	25	7	ADJ81346 Self-asse
10	64	38.6	28	8	ADQ43177 Peptide u
11	62.5	37.7	29	2	AA90178 Polycatio
12	62.5	37.7	29	2	AA90176 Polycatio
13	62.5	37.7	29	2	AAW06687 Protamine
14	62.5	37.7	29	2	AAW06697 Protamine
15	62	37.3	26	7	ABM18907 Flexible
16	61	36.7	29	2	AA90179 Polycatio
17	61	36.7	29	2	AAW06698 Protamine
18	57.5	34.6	27	6	ABR42885 Human his
19	57.5	34.6	28	2	AA90177 Polycatio
20	57.5	34.6	28	2	AAW06685 Protamine
21	57	34.3	30	3	AA808167 Peptide m
22	56	33.7	31	4	AA808450 Human pol
23	55	33.1	26	8	ADN11699 Peptide 1
24	54.5	32.8	31	2	AAW38224 NBC11 pep
25	54.5	32.8	32	3	AA808175 Peptide m

26	53	31.9	29	4	AA011831 Human pol
27	53	31.9	30	6	ABP59427 Self-asse
28	53	31.9	30	6	ABP59423 Self-asse
29	53	31.9	35	4	AA004715 Human pol
30	52	31.3	20	7	ADJ81345 Self-asse
31	52	31.3	20	7	ADJ81215 Self-asse
32	52	31.3	22	3	AB08176 Peptide m
33	52	31.3	30	5	AAE17118 Integrin-
34	52	31.3	30	6	ABP59422 Self-asse
35	52	31.3	31	4	AA011888 Human pol
36	51	30.7	18	2	AAW07290 Amphiphil
37	51	30.7	24	3	AA808171 Peptide m
38	51	30.7	33	4	AA004674 Human pol
39	50.5	30.4	29	3	AA808178 Peptide m
40	50.5	30.4	29	2	AA84173 Peptide e
41	50.5	30.4	33	5	ABG77360 Selected
42	50	30.1	21	4	AA8774630 21 mer pe
43	50	30.1	25	6	ABR42884 Human his
44	50	30.1	26	2	AAW03573 Compactin
45	50	30.1	28	2	AAW38882 Delivery

ALIGNMENTS

RESULT 1
AA82571
ID AA82571 standard; peptide; 35 AA.
XX
AC AA82571;
XX
DT 28-JUL-2000 (first entry)
XX
DB Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:1.
XX
KW Copolymer; molecular weight marker; TV-marker; immune disease;
KW Glutiramer acetate; autoimmune disease; anaphylactic; neuroprotective;
KW osteopathic; immunosuppressive; antithyroid; antinflammatory;
KW antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological;
KW antianemic; immunosuppressive; demyelinating disease; osteoarthritis;
KW inflammatory condition; multiple sclerosis; rheumatoid arthritis;
KW Crohn's disease; chronic immune thrombocytopenia purpura; colitis;
KW diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis;
KW Hashimoto's disease; idiopathic myxoedema; myasthenia Gravis;
KW pemphigus vulgaris; systemic lupus erythematosus.
OS Unidentified.
XX
FN WO200018794-A1.
XX
PD 06-APR-2000.
XX
PF 24-SEP-1999; 99WO-US022402.
XX
PR 25-SEP-1998; 98US-0101693P.
XX
PA (VEDA) YEDA RES & DEV CO LTD.
XX
PA (TEVA-) TEVA PHARM USA INC.
XX
FI Gad A, Lis D;
XX
XX WPI; 2000-317499/27.
PT Copolymer 1 related polypeptides used as molecular weight markers for
XX glatiramer acetate and for treatment and prevention of immune diseases.
XX
PS Claim 10; Page 14; 72pp; English.
XX
CC AA82571 to AA82577 represent specifically claimed copolymer molecular
XX weight TV-marker polypeptides from the present invention. The present
XX invention describes polypeptides (I) for determining the molecular weight
XX of a copolymer (CP), which has an identified molecular weight and an
XX amino acid composition corresponding to the copolymer. The polypeptides

of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune ophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, Crohn's disease, chronic immune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers

```

SQ      Sequence 35 AA;

Query Match      100.0%; Score 166; DB 3; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.1e-12;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AKKYAKKEKAANKAYKKEAKAKAAEAAKKAAYEA 35
         | | | | | | | | | | | | | | | | | | |
Db      1 AKKYAKKEKAANKAYKKEAKAKAAEAAKKAAYEA 35
         | | | | | | | | | | | | | | | | | | |

```

RESULT 2
ADN11701
ID ADN11701 standard; protein; 31 AA.
XX
XX ADN11701;
XX
XX
XX 15-JUL-2004 (first entry)
DT
XX
XX
DE Peptide linker SEQ ID NO: 38.
XX
XX
XX enzyme; Cre recombinase; chromosomal translocation; phage;
KW gene inactivation; transgenic; linker.
XX
OS Synthetic.

XX
PN
XX
XX
PD
XX
PF
XX
PR
XX
PA
EP1413586-A1.
28-APR-2004.
21-OCT-2002; 2002EP-00292603.
21-OCT-2002; 2002EP-00292603.
(CNRS) CNRS CENT NAT RECH SCI.

PI Herman J, Jullien NCG, Sampieri F;
XX
DR WPI; 2004-332811/31.
DR N-PSDB: ADN11700.

Use of nucleotide sequence encoding polypeptide sequence comprising
fragment of P1 bacteriophage Cre recombinase, vector containing
nucleotide sequence and polypeptide sequence for regulating P1
bacteriophage Cre recombinase activity.

PS Claim 15; Page 31; 51pp; English.

CC The present invention relates to the use of a first nucleotide sequence
CC encoding a first polypeptide sequence comprising N-terminal fragment of
CC p1 bacteriophage Cre recombinase, a second nucleotide sequence encoding
CC a second polypeptide sequence comprising C-terminal fragment of Cre
CC recombinase, a vector containing the first and second nucleotide sequences,
CC or first and second polypeptide sequences for regulating activity of p1
CC bacteriophage Cre recombinase. The sequences are useful for regulating
CC bacteriophage Cre recombinase.

CC the activity of the P1 bacteriophage Cre recombinase in cells, for
 CC inducing reciprocal chromosomal translocation, for exchanging one DNA
 CC cassette for another by recombinase-mediated cassette exchange and for
 CC the inactivation of selected genes in transgenic animals. The present
 CC sequence is a polypeptide shown in the exemplification of the invention.
 XX
 XX Sequence 31 AA;
 SQ

Query Match 42.8%; Score 71; DB 8; Length 31;
Best Local Similarity 64.5%; Pred. No. 0.21;
Matches 20; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

Qy 5 AKKEAAKAYKKEAKAKAAEAAAKEAAEYA 35
| | | | : | | | | | | | | : |
Dp 1 ASAEAAKEAAAKEAAAK--EAAKEAAAKA 29

RESULT 3
AAR90180
ID AAR90180 standard; peptide: 32 AA.

AA
AC AAR90180;

DT 25-MAR-1996 (first entry)

DE polycationic polypeptide n-protamine analogue.

XX n-protamine; anticoagulation reversal; low molecular weight heparin;
KW polycationic; positively charged amino acid; lysine.

AA Synthetic.

Key	Location/Qualifiers
Modified-site 1	
Modified-site 32	/note= "N-terminal is acetylated"
Modified-site	/note= "C-terminal is in amide form"

AA
PN
WO9513083-A1.

18-MAY-1995.

AA 10-NOV-1994; 94WO-US012981.
PF

AA 12-NOV-1993; 93US-00152488. PR

PK 08-SEP-1994; 3403-003030Z3.
XX

PA (UNMI) / UNIV MICHIGAN: XX

PI WAKERFIELD IW, STANLEY JC, ANDREWS FC,
XX

DR WPT; 1993-193899/23.
XX

P1 new poly:cationic polypeptide α -prolamine analogues - having reduced cationic charge and lower toxicity, used for reversing (low mol.wt.).

PT heparin anticoagulation.

PS Disclosure; Page 13; 34pp; English.

Novel peptides are claimed which contain 20-40 amino acids and which have a total cationic charge of less than +21 (pref. +16 to +18, esp. +18) as determined by the number of positively charged amino acids in the sequence. Preferably the positive charges are grouped in clusters separated by neutral amino acids. Especially the peptides contain 28-32 amino acids having blocks of 2-4 positively charged amino acids separated by blocks of 2-6 neutral acids. Alternatively the positive charge may be distributed evenly or randomly along the peptide sequence. In particular the peptides are analogues of α -protamine (total cationic charge = +21) in which selected arginine residues have been replaced with uncharged amino acids and other arginine residues have been replaced by other positively charged amino acid residues, preferably lysine. The peptides reverse the effect of low mol. wt. heparin (LMWH) anticoagulation and hence can be used medically to prevent bleeding after the conclusion of

Protamine sulphate (also called n-protamine or salmine protamine) is a polycationic peptide derived from salmon sperm and is used to reverse heparin anticoagulation. One of the major components of salmine protamine is a 32 amino acid peptide having a total cationic charge of [+21], with arginine accounting for 67% of the total sequence and for all of the positive charge. Peptides of 20-40 amino acids with total cationic charge less than [+21] and which are able, at least partially, to reverse the effect of heparin and/or low molecular weight heparin anticoagulants are claimed. Specifically, the peptides are polycationic analogues of n-protamine where the positive charge on the amino acid sequence is reduced by selective replacement of positively charged arginine residues with an uncharged residue, so that total cationic charge is less than [+21]. The

Query Match 40.7%; Score 67.5; DB 3; Length 32;

Best Local Similarity 62.1%; Pred. No. 0.55;
Matches 18; Conservative 4; Mismatches 4; Indels 3; Gaps 1;

QY 7 KEKAAYKKEKA---KAAEAKEAA 32
DB 2 RKKAARKAARKAARKAARKAARKAAR 30

RESULT 6

AAW06688
ID AAR90181 standard; peptide; 33 AA.

XX AC AAR90181;

XX DT 25-MAR-1996 (first entry)

XX DE Polycationic polypeptide n-protamine analogue.

XX KW n-protamine; anticoagulation reversal; low molecular weight heparin;
XX KW polycationic; positively charged amino acid; lysine.

XX OS Synthetic.

XX FH Key Location/Qualifiers
XX FT Modified-site 1 /note= "N-terminal is acetylated"
XX FT Modified-site 33 /note= "C-terminal is in amide form"

XX PN W09513083-A1.

XX PD 18-MAY-1995.

XX PX 10-NOV-1994; 94WO-US012981.

XX PR 12-NOV-1993; 93US-00152488.

XX PR 08-SEP-1994; 94US-00303025.

XX PA (UNMI) UNIV MICHIGAN.

XX PI Wakefield TW, Stanley JC, Andrews PC;

XX DR WPI; 1995-193899/25.

XX PT New poly:cationic polypeptide n-protamine analogues - having reduced
XX PT cationic charge and lower toxicity, used for reversing (low mol.wt.)
XX PT heparin anticoagulation.

XX PS Disclosure; Page 13; 34pp; English.

XX CC Novel peptides are claimed which contain 20-40 amino acids and which have
XX CC a total cationic charge of less than +21 (pref. +16 to +18; esp. +18) as
XX CC determined by the number of positively charged amino acids in the
XX CC sequence. Preferably the positive charges are grouped in clusters
XX CC separated by neutral amino acids. Especially the peptides contain 28-32
XX CC amino acids having blocks of 2-4 positively charged amino acids separated
XX CC by blocks of 2-6 neutral acids. Alternatively the positive charge may be
XX CC distributed evenly or randomly along the peptide sequence. In particular
XX CC the peptides are analogues of n-protamine (total cationic charge = +21)
XX CC in which selected arginine residues have been replaced with unchanged
XX CC amino acids and other arginine residues have been replaced by other
XX CC positively charged amino acid residues, preferably lysine. The peptides
XX CC reverse the effect of low mol. wt. heparin (LMWH) anticoagulation and
XX CC hence can be used medically to prevent bleeding after the conclusion of
XX CC clinical procedures using heparin therapy. They are less toxic than n-
XX CC protamine since the reduced positive charge gives an improved efficiency
XX CC to toxicity ratio; and they may be more effective than n-protamine in
XX CC their anti-LMWH action. The present sequence (total cationic charge =
XX CC +16) is a specific example of the new polypeptides

XX SQ Sequence 33 AA;

Query Match 40.7%; Score 67.5; DB 2; Length 33;

Best Local Similarity 61.3%; Pred. No. 0.57;
Matches 19; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 1 AKKAYK-EKAAYKKEKA---KAAEAKEAA 30
DB 3 AKKAYKKEKAARKAARKAARKAARKAAR 33

RESULT 7

AAW06688
ID AAW06688 standard; peptide; 33 AA.

XX AC AAW06688;

XX DT 05-AUG-1997 (first entry)

XX DE Protamine-like peptide analogue [+18BE].

XX KW Coagulation; anticoagulant; heparin; platelet aggregation; cell adhesion;
XX KW positively charged cluster; arginine; polycationic; decrease;
XX KW n-protamine; salmine protamine; protamine sulphate; salmon sperm.

XX OS Synthetic.

XX FH Key Location/Qualifiers
XX FT Modified-site 1 /note= "acetylated"
XX FT Region 4-31 /label= repeat_region
XX FT Modified-site 33 /note= "4 tandem repeats of (Lys)2(Ala)2(Lys)2Ala motif"
XX FT Modified-site 33 /note= "amidated"

XX PN W09635444-A1.

XX PD 14-NOV-1996.

XX PF 08-MAY-1996; 96WO-US006567.

XX PR 08-MAY-1995; 95US-00436703.

XX PA (UNMI) UNIV MICHIGAN.

XX PI Wakefield TW, Stanley JC, Andrews PC;

XX DR WPI; 1997-011697/01.

XX PT Peptide reversing the anticoagulant effects of heparin - is based on
XX PT protamine but has fewer positive charges for reduced toxicity.

XX PS Disclosure; Page 5; 42pp; English.

XX CC Protamine sulphate (also called n-protamine or salmine protamine) is a
XX CC polycationic peptide derived from salmon sperm and is used to reverse
XX CC heparin anticoagulation. One of the major components of salmine protamine
XX CC is a 32 amino acid peptide having a total cationic charge of [+21], with
XX CC arginine accounting for 67% of the total sequence and for all of the
XX CC positive charge. Peptides of 20-40 amino acids with total cationic charge
XX CC less than [+21] and which are able, at least partially, to reverse the
XX CC effect of heparin and/or low molecular weight heparin anticoagulants are
XX CC claimed. Specifically, the peptides are polycationic analogues of n-
XX CC protamine where the positive charge on the amino acid sequence is reduced
XX CC by selective replacement of positively charged arginine residues with an
XX CC unchanged residue, so that total cationic charge is less than [+21]. The
XX CC new peptides are used in vivo to reverse the effects of heparin; they
XX CC have the same anti-heparin activity as protamine but are less toxic
XX CC (because of the reduced number of positive charges) and are relatively
XX CC easy and inexpensive to prepare. The present sequence represents a
XX CC specific example of a protamine-like peptide with a charge of [+18] which
XX CC has been found to reverse the anticoagulation effects of both standard
XX CC and low molecular weight heparin

XX SQ Sequence 33 AA;

Query Match 40.7%; Score 67.5; DB 2; Length 33;
 Best Local Similarity 61.3%; Pred. No. 0.57;
 Matches 19; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 1 AKKAKK-EKAAKAYKKEAKAAEAAAKE 30
 DB 3 AKKAKKAKKAKKAKKAKKAKKAKKAKK 33

RESULT 8
 ADJ81216
 ID ADJ81216 standard; peptide; 25 AA.

AC ADJ81216;
 DT 06-MAY-2004 (first entry)

DE Self-assembling polymer peptide #71.

XX miniblock polymer; optical response; mid infrared wavelength range;
 KW long range ordered fluid; liquid crystals; nanolithography;
 KW IR-sensitive device; IR sensor; IR filter; night telescope;
 KW thermosensitive detector; non-linear chromophore; biomaterial;
 KW tissue engineering scaffold; ferroelectric material; artificial muscle;
 KW switching device.

XX Synthetic.

XX WO2003056297-A2.

XX 10-JUL-2003.

XX 02-OCT-2002; 2002WO-US031375.

XX 02-OCT-2001; 2001US-0326743P.

XX 04-JUN-2002; 2002US-0385809P.

XX (TUFT) TUFTS COLLEGE.

XX Valluzzi R, Kaplan DL;

XX WPI; 2003-671392/63.

XX Miniblock polymer useful in nanolithographic processes, has self-fabricating block and solubilizing block, has glycine and self-fabricates to form 3-dimensional materials having long-range orders, in solution.

XX Claim 31; SEQ ID NO 71; 91pp; English.

XX The invention relates to a miniblock polymer (I) comprising a self-fabricating block and a solubilizing block, a block for triggering self-fabrication by external or environmental conditions, and a block for incorporating turns in the polymer or for providing sites for chemical modifications, has a molecular weight of 1000-300000 and, in solution, can self-fabricate to form 3-dimensional material having long-range order, and where (I) has glycine content of at least 20%. (I) is useful for controlled delivery of a drug which involves incorporating a drug within (I), and administering the self-fabricating material incorporating the drug. The drug is incorporated within layers of the self-fabricating material. (II) is useful for modifying the optical response of a device in the near to mid infrared wavelength range which involves applying (II) to the surface of the device (all claimed). (I) is useful for preparing long range ordered fluids (i.e., liquid crystals) in a variety of phases or forms, which can then undergo very specific structural transitions to form rigid materials. (I) can be used as structural tissue implants, in liquid crystal displays, and for producing high-performance composites. (I) is useful for preparing chemically patterned templates with either general features are specific features. (I) is also useful in nanolithographic processes. A self-fabricated structure containing the polymer (II) is useful for modifying and improving performance of IR-sensitive devices, IR sensors, IR filters, night telescopes and thermosensitive detectors. (II) can be used for preparing films,

CC membranes or coatings that absorb specific wavelengths of infrared radiation, and in optical applications e.g., as matrices to align non-linear chromophores which are useful in creating materials for second order non-linear optics. (II) is useful in hydrogen catalysis, as coatings for biomaterials, scaffolds for tissue engineering, ferroelectric materials, artificial muscles, switching devices, etc. This sequence represents a peptide used in the method of the invention.

XX Sequence 25 AA;

Query Match 39.2%; Score 65; DB 7; Length 25;
 Best Local Similarity 72.0%; Pred. No. 0.84;
 Matches 18; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

QY 8 EKAACKAYKKEAKAAEAAAKEAA 32
 DB 1 EAAAKEAAKEAAK--EAAAKEAA 23

RESULT 9

ADJ81346

ID ADJ81346 standard; peptide; 25 AA.

AC ADJ81346;

DT 06-MAY-2004 (first entry)

DE Self-assembling polymer peptide #201.

XX miniblock polymer; optical response; mid infrared wavelength range;
 KW long range ordered fluid; liquid crystals; nanolithography;
 KW IR-sensitive device; IR sensor; IR filter; night telescope;
 KW thermosensitive detector; non-linear chromophore; biomaterial;
 KW tissue engineering scaffold; ferroelectric material; artificial muscle;
 KW switching device.

XX Synthetic.

XX WO2003056297-A2.

XX 10-JUL-2003.

XX 02-OCT-2002; 2002WO-US031375.

XX 02-OCT-2001; 2001US-0326743P.

XX 04-JUN-2002; 2002US-0385809P.

XX (TUFT) TUFTS COLLEGE.

XX Valluzzi R, Kaplan DL;

XX WPI; 2003-671392/63.

XX Miniblock polymer useful in nanolithographic processes, has self-fabricating block and solubilizing block, has glycine and self-fabricates to form 3-dimensional materials having long-range orders, in solution.

XX Disclosure; SEQ ID NO 202; 91pp; English.

XX The invention relates to a miniblock polymer (I) comprising a self-fabricating block and a solubilizing block, a block for triggering self-fabrication by external or environmental conditions, and a block for incorporating turns in the polymer or for providing sites for chemical modifications, has a molecular weight of 1000-300000 and, in solution, can self-fabricate to form 3-dimensional material having long-range order, and where (I) has glycine content of at least 20%. (I) is useful for controlled delivery of a drug which involves incorporating a drug within (I), and administering the self-fabricating material incorporating the drug. The drug is incorporated within layers of the self-fabricating material. (II) is useful for modifying the optical response of a device in the near to mid infrared wavelength range which involves applying (II) to the surface of the device (all claimed). (I) is useful for preparing long range ordered fluids (i.e., liquid crystals) in a variety of phases

The present sequence is that of a peptide of potential use for production of a coded probe useful in the method of the invention. The invention provides methods, apparatus and compositions for the detection, identification and/or sequencing of biomolecules, such as nucleic acids or proteins. Coded probes comprising a probe molecule attached to one or more nano-barcodes are allowed to bind to target molecule(s). After binding and separation from unbound coded probes, the bound coded probes are aligned on a surface and analysed by scanning probe microscopy (SPM). The methods allow the sequencing of long nucleic acid sequences in a single sequencing run, high speed of obtaining sequence data, low cost of

CC to toxicity ratio; and they may be more effective than n-protamine in
 CC their anti-LMW action. The present sequence (total cationic charge =
 CC +16) is a specific example of the new polypeptides
 XX
 SQ Sequence 29 AA;

Query Match 37.7%; Score 62.5; DB 2; Length 29;
 Best Local Similarity 62.1%; Pred. No. 1.9;
 Matches 18; Conservative 1; Mismatches 9; Indels 1; Gaps 1;

QY 1 AKKYAKKEKAAYKKEAKAKAEAAK 29
 ||| ||| ||| ||| ||| ||| ||| |||
 Db 2 AKKAACKKAACKKAACK-KAKKAACK 29

RESULT 12
 AAR90176
 ID AAR90176 standard; peptide; 29 AA.

XX AAR90176;
 XX 25-MAR-1996 (first entry)
 XX Polycationic polypeptide n-protamine analogue.

XX n-protamine; anticoagulation reversal; low molecular weight heparin;
 KW polycationic; positively charged amino acid; lysine.
 XX
 OS Synthetic.

FH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal can be acetylated"
 FT Modified-site 29 /note= "C-terminal can be in amide form"

XX W09513083-A1.
 XX 18-MAY-1995.
 XX 10-NOV-1994; 94WO-US012981.
 XX 12-NOV-1993; 93US-00152488.
 PR 08-SEP-1994; 94US-00303025.
 XX
 PA (UNMI) UNIV MICHIGAN.

XX Wakefield TW, Stanley JC, Andrews PC;
 PI WPI; 1995-193899/25.

XX New poly:cationic polypeptide n-protamine analogues - having reduced
 PT cationic charge and lower toxicity, used for reversing (low mol.wt.)
 PT heparin anticoagulation.

XX Disclosure; Page 13; 34pp; English.

XX Novel peptides are claimed which contain 20-40 amino acids and which have
 CC a total cationic charge of less than +21 (pref. +16 to +18; esp. +18) as
 CC determined by the number of positively charged amino acids in the
 CC sequence. Preferably the positive charges are grouped in clusters
 CC separated by neutral amino acids. Especially the peptides contain 28-32
 CC amino acids having blocks of 2-4 positively charged amino acids separated
 CC by blocks of 2-6 neutral acids. Alternatively the positive charge may be
 CC distributed evenly or randomly along the peptide sequence. In particular
 CC the peptides are analogues of n-protamine (total cationic charge = +21)
 CC in which selected arginine residues have been replaced with uncharged
 CC amino acids and other arginine residues have been replaced by other
 CC positively charged amino acid residues, preferably lysine. The peptides
 CC reverse the effect of low mol. wt. heparin (LMWH) anticoagulation and
 CC hence can be used medically to prevent bleeding after the conclusion of
 CC clinical procedures using heparin therapy. They are less toxic than n-
 CC protamine since the reduced positive charge gives an improved efficiency

CC to toxicity ratio; and they may be more effective than n-protamine in
 CC their anti-LMW action. The present sequence (total cationic charge =
 CC +16) is a specific example of the new polypeptides
 XX
 SQ Sequence 29 AA;

Query Match 37.7%; Score 62.5; DB 2; Length 29;
 Best Local Similarity 62.1%; Pred. No. 1.9;
 Matches 18; Conservative 1; Mismatches 9; Indels 1; Gaps 1;

QY 1 AKKYAKKEKAAYKKEAKAKAEAAK 29
 ||| ||| ||| ||| ||| ||| ||| |||
 Db 2 AKKAACKKAACKKAACK-KAKKAACK 29

RESULT 13
 AAW06687
 ID AAW06687 standard; peptide; 29 AA.

XX AAW06687;
 XX 05-AUG-1997 (first entry)
 XX Protamine-like peptide analogue [+16BE].

XX Coagulation; anticoagulant; heparin; platelet aggregation; cell adhesion;
 KW positively charged cluster; arginine; polycationic; decrease;
 KW n-protamine; saline protamine; protamine sulphate; salmon sperm.
 XX
 OS Synthetic.

FH Key Location/Qualifiers
 FT Modified-site 1 /note= "acetylated"
 FT Region 2. .29 /label= repeat region
 FT Modified-site 29 /note= "4 tandem repeats of Ala(Lys)2(Ala)2(Lys)2 motif"
 FT Modified-site 29 /note= "amidated"

XX W09635444-A1.
 XX 14-NOV-1996.
 XX 08-MAY-1996; 96WO-US006567.
 XX 08-MAY-1995; 95US-00436703.
 XX (UNMI) UNIV MICHIGAN.

XX Wakefield TW, Stanley JC, Andrews PC;
 PI WPI; 1997-011697/01.

XX Peptide reversing the anticoagulant effects of heparin - is based on
 PT protamine but has fewer positive charges for reduced toxicity.

XX Disclosure; Page 5; 42pp; English.

XX Protamine sulphate (also called n-protamine or saline protamine) is a
 CC polycationic peptide derived from salmon sperm and is used to reverse
 CC heparin anticoagulation. One of the major components of saline protamine
 CC is a 32 amino acid peptide having a total cationic charge of [+21], with
 CC arginine accounting for 67% of the total sequence and for all of the
 CC positive charge. Peptides of 20-40 amino acids with total cationic charge
 CC less than [+21] and which are able, at least partially, to reverse the
 CC effect of heparin and/or low molecular weight heparin anticoagulants are
 CC claimed. Specifically, the peptides are polycationic analogues of n-
 CC protamine where the positive charge on the amino acid sequence is reduced
 CC by selective replacement of positively charged arginine residues with an
 CC uncharged residue, so that total cationic charge is less than [+21]. The
 CC new peptides are used in vivo to reverse the effects of heparin; they
 CC have the same anti-heparin activity as protamine but are less toxic

CC (because of the reduced number of positive charges) and are relatively
 CC easy and inexpensive to prepare. The present sequence represents a
 CC specific example of a protamine-like peptide with a charge of [+16] which
 CC has been found to reverse the anticoagulation effects of both standard
 CC and low molecular weight heparin
 XX
 SQ Sequence 29 AA;

Query Match 37.7%; Score 62.5; DB 2; Length 29;
 Best Local Similarity 62.1%; Pred. No. 1.9;
 Matches 18; Conservative 1; Mismatches 9; Indels 1; Gaps 1;
 Qy 1 AKKYAKKEKAAYKKEAKAKAEAAAK 29
 ||| ||| ||| ||| ||| ||| ||| :|||
 Db 2 AKKAACKAKKAAYKKEAKAK-KAKKAACK 29

RESULT 14
 AAW06697
 ID AAW06697 standard; peptide; 29 AA.
 XX
 AC AAW06697;
 DT 06-AUG-1997 (first entry)
 XX
 DE Protamine-like peptide analogue P(AK2A2K2)4 with a charge of [+16].
 XX
 KW Coagulation; anticoagulant; heparin; platelet aggregation; cell adhesion;
 KW positively charged cluster; arginine; polycationic; decrease;
 KW n-protamine; salmine protamine; protamine sulphate; salmon sperm.
 XX
 OS Synthetic.
 XX

Key Location/Qualifiers
 FT Modified-site 1 /note= "acetylated if C-terminus is amidated"
 FT Region 2. 29 /label= repeat region
 FT Modified-site 29 /note= "4 tandem repeats of Ala(Lys)2(Ala)2(Lys)2 motif"
 FT Modified-site 29 /note= "amidated if N-terminus is acetylated"
 XX
 FN WO9635444-A1.
 XX
 PD 14-NOV-1996.
 XX
 PF 08-MAY-1996; 96WO-US006567.
 XX
 PR 08-MAY-1995; 95US-00436703.
 XX
 PA (UNWI) UNIV MICHIGAN.
 XX
 PI Wakefield TW, Stanley JC, Andrews PC;
 XX
 DR WPI; 1997-011697/01.

XX
 XX Peptide reversing the anticoagulant effects of heparin - is based on
 PT protamine but has fewer positive charges for reduced toxicity.
 PT
 PS Disclosure; Page 13; 42pp; English.

XX
 CC Protamine sulphate (also called n-protamine or salmine protamine) is a
 CC polycationic peptide derived from salmon sperm and is used to reverse
 CC heparin anticoagulation. One of the major components of salmine protamine
 CC is a 32 amino acid peptide having a total cationic charge of [+21], with
 CC arginine accounting for 67% of the total sequence and for all of the
 CC positive charge. Peptides of 20-40 amino acids with total cationic charge
 CC less than [+21] and which are able, at least partially, to reverse the
 CC effect of heparin and/or low molecular weight heparin anticoagulants are
 CC claimed. Specifically, the peptides are polycationic analogues of n-
 CC protamine where the positive charge on the amino acid sequence is reduced
 CC by selective replacement of positively charged arginine residues with an
 CC uncharged residue, so that total cationic charge is less than [+21]. The

CC new peptides are used in vivo to reverse the effects of heparin; they
 CC have the same anti-heparin activity as protamine but are less toxic
 CC (because of the reduced number of positive charges) and are relatively
 CC easy and inexpensive to prepare. The present sequence represents a
 CC specific example of a protamine-like peptide with a charge of [+16] which
 CC has been found to reverse the anticoagulation effects of both standard
 CC and low molecular weight heparin
 XX
 SQ Sequence 29 AA;

Query Match 37.7%; Score 62.5; DB 2; Length 29;
 Best Local Similarity 62.1%; Pred. No. 1.9;
 Matches 18; Conservative 1; Mismatches 9; Indels 1; Gaps 1;
 Qy 1 AKKYAKKEKAAYKKEAKAKAEAAAK 29
 ||| ||| ||| ||| ||| ||| ||| :|||
 Db 2 AKKAACKAKKAAYKKEAKAK-KAKKAACK 29

RESULT 15
 ABM18907
 ID ABM18907 standard; peptide; 26 AA.
 XX
 AC ABM18907;
 DT 13-OCT-2003 (first entry)
 XX
 DE Flexible linker peptide L1.
 XX
 KW antibacterial; antiinflammatory; auditory; vaccine; meningitis;
 KW streptococcal infection; otitis media; bacteraemia; pneumonia; linker.
 XX
 OS Synthetic.
 XX
 FN WO2003054007-A2.
 XX
 PD 03-JUL-2003.
 XX
 PF 20-DEC-2002; 2002WO-CA002006.
 XX
 PR 20-DEC-2001; 2001US-0341252P.
 XX
 PA (SHIR-) SHIRE BIOCHEM INC.
 XX
 PI Hamel J, Charland N, Brodeur BR, Martin D, Blais N, Ouellet C;
 PI Labbe S;
 XX
 DR WPI; 2003-569224/53.

XX
 XX New isolated polypeptides of Streptococcus pneumoniae, useful for
 PT diagnosing, preventing or treating streptococcal infection, meningitis,
 PT otitis media, bacteraemia or pneumonia infection.
 XX
 PS Example 9; Page 51; 79pp; English.

XX
 CC The invention relates to a novel isolated polypeptide of Streptococcus
 CC pneumoniae. A polypeptide of the invention has antibacterial,
 CC antiinflammatory, and auditory activity, and is used as a vaccine. The
 CC polypeptide or pharmaceutical composition is useful for the prophylactic
 CC or therapeutic treatment of streptococcal infection, meningitis, otitis
 CC media, bacteraemia or pneumonia infection. The kit is useful for
 CC detecting or diagnosing streptococcal infection. The pharmaceutical
 CC composition is useful as a vaccine. The polynucleotides are useful in
 CC designing DNA probes for detecting circulating Streptococcus in a
 CC biological sample. The present sequence is used in the exemplification of
 CC the invention. Note: The sequence data for this patent is not fully
 CC represented in the printed specification, but is based on sequence
 CC information supplied by the European Patent Office
 XX
 SQ Sequence 26 AA;

Query Match 37.3%; Score 62; DB 7; Length 26;
 Best Local Similarity 68.0%; Pred. No. 1.9;

Matches 17; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

Qy 8 EKAAYKAYKAKAAEAAKEAA 32

Db : |||: ||| || |||||

2 DAAAKEAAAKEAAK--EAAKEAA 24

Search completed: June 3, 2005, 09:56:50
Job time : 160 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2005, 09:57:01 ; Search time 138 Seconds
(without alignments)

87,672 Million cell updates/sec

Title: US-10-792-311-1

Perfect score: 166

Sequence: 1 AKKYAKKEKAAYKAYKKEAKAKAAEAAYEA 35

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1465611 seqs, 345679903 residues

Total number of hits satisfying chosen parameters: 373443

Minimum DB seq length: 0

Maximum DB seq length: 35

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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12: /cgn2_6/ptodata/1/pubaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	166	100.0	35	9	US-09-816-989A-1
2	166	100.0	35	17	US-10-792-311-1
3	65	39.2	25	17	US-10-490-799-71
4	64	38.6	28	16	US-10-667-004-21
5	62	37.3	26	15	US-10-324-143-119
6	57.5	34.6	27	10	US-09-988-165B-7
7	53	31.9	30	14	US-10-192-832-69
8	53	31.9	30	14	US-10-192-832-73
9	52	31.3	30	17	US-10-490-799-70
10	52	31.3	30	14	US-10-192-832-68
11	52	31.3	35	15	US-10-424-599-241097
12	51	30.7	34	16	US-10-437-963-160178
13	50	30.1	21	17	US-10-909-119-128
					Sequence 1, Appli
					Sequence 1, Appli
					Sequence 71, Appl
					Sequence 119, App
					Sequence 7, Appli
					Sequence 69, Appl
					Sequence 73, Appl
					Sequence 70, Appl
					Sequence 68, Appl
					Sequence 241097,
					Sequence 160178,
					Sequence 128, App

14	50	30.1	25	10	US-09-988-165B-6	Sequence 6, Appli
15	50	30.1	28	9	US-09-805-301-22	Sequence 22, Appl
16	50	30.1	29	9	US-09-805-301-23	Sequence 23, Appl
17	50	30.1	30	9	US-09-805-301-24	Sequence 24, Appl
18	50	30.1	30	15	US-10-308-322-2	Sequence 2, Appli
19	50	30.1	31	9	US-09-805-301-25	Sequence 25, Appl
20	50	30.1	32	9	US-09-805-301-26	Sequence 26, Appl
21	50	30.1	33	9	US-09-805-301-27	Sequence 27, Appl
22	50	30.1	33	9	US-09-805-301-121	Sequence 121, App
23	50	30.1	34	9	US-09-805-301-28	Sequence 28, Appl
24	50	30.1	34	9	US-09-805-301-122	Sequence 122, App
25	50	30.1	35	9	US-09-805-301-29	Sequence 29, Appl
26	50	30.1	35	9	US-09-805-301-123	Sequence 123, App
27	50	30.1	35	15	US-10-424-599-198091	Sequence 198091,
28	49	29.5	28	9	US-09-805-301-60	Sequence 60, Appl
29	49	29.5	29	9	US-09-805-301-61	Sequence 61, Appl
30	49	29.5	30	9	US-09-124-280A-2	Sequence 2, Appli
31	49	29.5	30	9	US-09-805-301-62	Sequence 62, Appl
32	49	29.5	30	15	US-10-424-599-163624	Sequence 163624,
33	49	29.5	31	9	US-09-805-301-63	Sequence 63, Appl
34	49	29.5	31	9	US-09-805-301-119	Sequence 119, App
35	49	29.5	31	15	US-10-296-879-26	Sequence 26, Appl
36	49	29.5	31	16	US-10-471-895-15	Sequence 15, Appl
37	49	29.5	32	9	US-09-805-301-64	Sequence 64, Appl
38	49	29.5	32	9	US-09-805-301-120	Sequence 120, App
39	49	29.5	33	9	US-09-805-301-65	Sequence 65, Appl
40	49	29.5	34	9	US-09-805-301-66	Sequence 66, Appl
41	49	29.5	35	9	US-09-805-301-67	Sequence 67, Appl
42	49	29.5	35	15	US-10-424-599-236809	Sequence 236809,
43	49	29.5	35	15	US-10-424-599-272273	Sequence 272273,
44	49	29.5	35	15	US-10-333-313-4	Sequence 4, Appli
45	48.5	29.2	28	16	US-10-667-004-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1

US-09-816-989A-1

; Sequence 1, Application US/09816989A

; Patent No. US20020115103A1

; GENERAL INFORMATION:

; APPLICANT: Gad, Alexander

; APPLICANT: Lis, Doris

; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI

; FILE REFERENCE: 2609/60807-A-PCT-US

; CURRENT APPLICATION NUMBER: US/09/816,989A

; CURRENT FILING DATE: 2001-03-23

; PRIOR APPLICATION NUMBER: 60/101,693

; PRIOR FILING DATE: 1998-09-25

; PRIOR APPLICATION NUMBER: PCT/US99/22402

; PRIOR FILING DATE: 1999-09-24

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 35

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-1

Query Match

Best Local Similarity 100.0%; Score 166; DB 9; Length 35;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AKKYAKKEKAAYKAYKKEAKAKAAEAAYEA 35

Db 1 AKKYAKKEKAAYKAYKKEAKAKAAEAAYEA 35

RESULT 2

US-10-792-311-1
; Sequence 1, Application US/10792311
; Publication No. US20050038233A1
; GENERAL INFORMATION:
; APPLICANT: Gad, Alexander
; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
; TITLE OF INVENTION: AND FOR THERAPEUTIC USE
; FILE REFERENCE: 2609/60807-A-PCT-US
; CURRENT APPLICATION NUMBER: US/10/792,311
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/09/816,989
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/101,693
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22402
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-10-792-311-1

Query Match 100.0%; Score 166; DB 17; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.7e-11;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKYAKEKAAKAYKKEAKAKAAEAAAKEAAEA 35
Db 1 AKYAKEKAAKAYKKEAKAKAAEAAAKEAAEA 35

RESULT 3
US-10-490-799-71
; Sequence 71, Application US/10490799
; Publication No. US20050090641A1
; GENERAL INFORMATION:
; APPLICANT: VALLUZZI, REGINA
; APPLICANT: KAPLAN, DAVID
; TITLE OF INVENTION: SELF-ASSEMBLING POLYMERS, AND MATERIALS FABRICATED
; TITLE OF INVENTION: THEREFROM
; FILE REFERENCE: TUV-029.01
; CURRENT APPLICATION NUMBER: US/10/490,799
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: PCT/US02/31375
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/326,743
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/385,809
; PRIOR FILING DATE: 2002-06-04
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-490-799-71

Query Match 39.2%; Score 65; DB 17; Length 25;
Best Local Similarity 72.0%; Pred. No. 1.3;
Matches 18; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

Qy 8 EKAACKAYKKEAKAAEAAAKEAA 32
Db 1 EAAAKEAAAKEAAK--EAAAKEAA 23

RESULT 4
US-10-667-004-21
; Sequence 21, Application US/10667004
; Publication No. US20040126820A1
; GENERAL INFORMATION:
; APPLICANT: INTEL CORPORATION
; APPLICANT: CHAN, Selena
; APPLICANT: SU, Xing
; APPLICANT: YAMAKAWA, Mineo
; TITLE OF INVENTION: CONTROLLED ALIGNMENT OF NANO-BARCODES ENCODING SPECIFIC INFORMATION
; TITLE OF INVENTION: SCANNING PROBE MICROSCOPY (SPM)
; FILE REFERENCE: INTEL1310-1(P14240X)
; CURRENT APPLICATION NUMBER: US/10/667,004
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US 10/251,152
; PRIOR FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-667-004-21

Query Match 38.6%; Score 64; DB 16; Length 28;
Best Local Similarity 65.5%; Pred. No. 1.9;
Matches 19; Conservative 1; Mismatches 7; Indels 2; Gaps 1;

Qy 1 AKYAKEKAAKAYKKEAKAKAAEAAAK 29
Db 2 AKAANKAAKAAKAAK--AAKAAKAAK 28

RESULT 5
US-10-324-143-119
; Sequence 119, Application US/10324143
; Publication No. US20030232976A1
; GENERAL INFORMATION:
; APPLICANT: HAMEL, JOSEF
; APPLICANT: CHARLAND, NATHALIE
; APPLICANT: BRODEUR, BERNARD R.
; APPLICANT: MARTIN, DENIS
; APPLICANT: BLAIS, NORMAND
; APPLICANT: OUELETTE, CATHERINE
; TITLE OF INVENTION: STREPTOCOCCUS ANTIGENS
; FILE REFERENCE: 55190-56
; CURRENT APPLICATION NUMBER: US/10/324,143
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 60/341,252
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 119
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: linker peptide
US-10-324-143-119

Query Match 37.3%; Score 62; DB 15; Length 26;
Best Local Similarity 68.0%; Pred. No. 2.9;
Matches 17; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

Qy 8 EKAACKAYKKEAKAAEAAAKEAA 32
Db 2 DAAAKEAAAKEAAK--EAAAKEAA 24


```
RESULT 6
US-09-988-165B-7
; Sequence 7, Application US/09988165B
; Publication No. US20030144473A1
; GENERAL INFORMATION:
; APPLICANT: Symbiotec Gesellschaft zur Erforschung und Entwicklung
; APPLICANT: auf dem Gebiet der Biotechnologie mbH
; TITLE OF INVENTION: Peptides for the Production of Preparations
; TITLE OF INVENTION: Peptides for the Diagnosis and Therapy of Autoimmune Diseases
; FILE REFERENCE: 3642
; CURRENT APPLICATION NUMBER: US/09/988,165B
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US Serial Number 07/946,180
; PRIOR FILING DATE: 1992-09-16
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 7
; LENGTH: 27
; TYPE: PRT
; ORGANISM: human
US-09-988-165B-7

Query Match      34.6%; Score 57.5; DB 10; Length 27;
Best Local Similarity 56.7%; Pred. No. 9.4;
Matches 17; Conservative 2; Mismatches 8; Indels 3; Gaps 1;

Qy 2 KKYAKKEAAKAYKKEAKAAEAEEAAKEA 31
Db 1 KPKAAKPKAAK---PKAAKPKAAKAAKKA 27

RESULT 7
US-10-192-832-69
; Sequence 69, Application US/10192832
; Publication No. US20030176335A1
; GENERAL INFORMATION:
; APPLICANT: ZHANG, SHUGUANG
; APPLICANT: VAUTHEY, SYLVAIN
; TITLE OF INVENTION: SURFACTANT PEPTIDE NANOSTRUCTURES, AND USES THEREOF.
; FILE REFERENCE: MTV-043.01
; CURRENT APPLICATION NUMBER: US/10/192,832
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 60/304,256
; PRIOR FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 69
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-192-832-69

Query Match      31.9%; Score 53; DB 14; Length 30;
Best Local Similarity 60.9%; Pred. No. 33;
Matches 14; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 10 AAKKAYKKEAKAAEAEEAAKAA 32
Db 8 AAKKKKKKKKAAAAAAAAAAAA 30

RESULT 8
US-10-192-832-73
; Sequence 73, Application US/10192832
; Publication No. US20030176335A1
; GENERAL INFORMATION:
; APPLICANT: ZHANG, SHUGUANG
; APPLICANT: VAUTHEY, SYLVAIN
; TITLE OF INVENTION: SURFACTANT PEPTIDE NANOSTRUCTURES, AND USES THEREOF
; FILE REFERENCE: MTV-043.01
; CURRENT APPLICATION NUMBER: US/10/192,832
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 60/304,256
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; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 60/304,256
; PRIOR FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 73
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-192-832-73

Query Match      31.9%; Score 53; DB 14; Length 30;
Best Local Similarity 53.8%; Pred. No. 33;
Matches 14; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

Qy 9 KAAKAYKKEAKAAEAEEAAKAAVE 34
Db 1 KKKKKKKKAAAAAAAAAAAAEEEEE 26

RESULT 9
US-10-430-799-70
; Sequence 70, Application US/10490799
; Publication No. US20050090641A1
; GENERAL INFORMATION:
; APPLICANT: VALLUZZI, REGINA
; APPLICANT: KAPLAN, DAVID
; TITLE OF INVENTION: SELF-ASSEMBLING POLYMERS, AND MATERIALS FABRICATED
; TITLE OF INVENTION: THEREFROM
; FILE REFERENCE: TUV-029.01
; CURRENT APPLICATION NUMBER: US/10/490,799
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: PCT/US02/31375
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/326,743
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/385,809
; PRIOR FILING DATE: 2002-06-04
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-430-799-70

Query Match      31.3%; Score 52; DB 17; Length 20;
Best Local Similarity 68.2%; Pred. No. 28;
Matches 15; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

Qy 8 EKAACKAYKKEAKAAEAEEAAK 29
Db 1 EAAAKEAAKAAK--EAAAK 20

RESULT 10
US-10-192-832-68
; Sequence 68, Application US/10192832
; Publication No. US20030176335A1
; GENERAL INFORMATION:
; APPLICANT: ZHANG, SHUGUANG
; APPLICANT: VAUTHEY, SYLVAIN
; TITLE OF INVENTION: SURFACTANT PEPTIDE NANOSTRUCTURES, AND USES THEREOF
; FILE REFERENCE: MTV-043.01
; CURRENT APPLICATION NUMBER: US/10/192,832
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 60/304,256
```



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; PRIOR FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 68
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-192-832-68

Query Match          31.3%; Score 52; DB 14; Length 30;
Best Local Similarity 59.1%; Pred. No. 42;
Matches 13; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 9 KAAYKAYKEKAKAAAEAAAKE 30
Db 1 KKKKKKKKKKAAAEAAAKK 22

RESULT 11
US-10-424-599-241097
; Sequence 241097, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 241097
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_59739C.1.pep
US-10-424-599-241097

Query Match          31.3%; Score 52; DB 15; Length 35;
Best Local Similarity 60.0%; Pred. No. 49;
Matches 12; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 2 KKYAKKEKAAKAYKEAKA 21
Db 16 KKKKKKKKKKSYIKKYKA 35

RESULT 12
US-10-437-963-160178
; Sequence 160178, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 160178
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; LENGTH: 34
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_59481C.1.pep
US-10-437-963-160178

Query Match          30.7%; Score 51; DB 16; Length 34;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 12; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 2 KKYAKKEKAAKAYKEAKAK 22
Db 6 KKKKKKKKKKKKKKKKKK 26

RESULT 13
US-10-909-119-128
; Sequence 128, Application US/10909119
; Publication No. US20050079578A1
; GENERAL INFORMATION:
; APPLICANT: Centanni, John M.
; APPLICANT: Allen-Hoffmann, Lynn
; TITLE OF INVENTION: Human Skin Equivalents Expressing Exogenous Polypeptides
; FILE REFERENCE: STRATA-09123
; CURRENT APPLICATION NUMBER: US/10/909,119
; CURRENT FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 128
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: MISC FEATURE
; LOCATION: (8)..(21)
; OTHER INFORMATION: The residues at these positions may be present or absent.
US-10-909-119-128

Query Match          30.1%; Score 50; DB 17; Length 21;
Best Local Similarity 65.2%; Pred. No. 48;
Matches 15; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

Qy 9 KAARKAYKEAKAKAAEAARKEA 31
Db 1 KAARKAAK--AAKKAARAKAA 21

RESULT 14
US-09-988-165B-6
; Sequence 6, Application US/09988165B
; Publication No. US20030144473A1
; GENERAL INFORMATION:
; APPLICANT: Symbiotec Gesellschaft zur Erforschung und Entwicklung
; APPLICANT: auf dem Gebiet der Biotechnologie mbH
; TITLE OF INVENTION: Peptides for the Production of Preparations
; TITLE OF INVENTION: for the Diagnosis and Therapy of Autoimmune Diseases
; FILE REFERENCE: 3642
; CURRENT APPLICATION NUMBER: US/09/988,165B
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US Serial Number 07/946,180
; PRIOR FILING DATE: 1992-09-16
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 6
; LENGTH: 25
; TYPE: PRT
; ORGANISM: human
US-09-988-165B-6

Query Match          30.1%; Score 50; DB 10; Length 25;
Best Local Similarity 54.2%; Pred. No. 58;
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Matches 13; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Qy 7 KEKAAKAYKEAKAAAEAAAKE 30
 Db 1 KPAAKPKAAKPKAAKAAKAAK 24

RESULT 15

US-09-805-301-22
 ; Sequence 22, Application US/09805301
 ; Patent No. US20020173456A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Smith, Louis C.
 ; Sparrow, James T.
 ; Hauer, Jochen
 ; Mims, Martha P.
 ; TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
 ; MACROMOLECULE DELIVERY
 ; NUMBER OF SEQUENCES: 139
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 6.0
 ; SOFTWARE: Word Perfect 6.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/805,301
 ; FILING DATE: 12-Mar-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/584,043
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard J.
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 217/189
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 22:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 28 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
 US-09-805-301-22

Query Match 30.1%; Score 50; DB 9; Length 28;
 Best Local Similarity 42.9%; Pred. No. 65;
 Matches 12; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

Qy 2 KKYAKKEKAAKAYKEAKAAAEAAAK 29
 Db 1 KKKKKKKKKKKKKKKKKKKKKKKVTK 28

Search completed: June 3, 2005, 10:11:47
 Job time : 139 secs

This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2005, 09:48:15 ; Search time 41 Seconds
(without alignments)
63.725 Million cell updates/sec

Title: US-10-792-311-1
Perfect score: 166
Sequence: 1 AKKYAKKEKAAYKKEAKAARAAKAAAYEA 35

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 250370

Minimum DB seq length: 0
Maximum DB seq length: 35

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	166	100.0	35	4	US-09-405-743A-1
2	166	100.0	35	4	US-09-816-989A-1
3	67.5	40.7	32	1	US-08-152-488-13
4	67.5	40.7	32	1	US-08-303-025-15
5	67.5	40.7	32	1	US-08-677-304-13
6	67.5	40.7	32	2	US-08-436-703B-2
7	67.5	40.7	33	1	US-08-303-025-16
8	67.5	40.7	33	2	US-08-436-703B-4
9	62.5	37.7	29	1	US-08-152-488-10
10	62.5	37.7	29	1	US-08-152-488-11
11	62.5	37.7	29	1	US-08-303-025-10
12	62.5	37.7	29	1	US-08-303-025-11
13	62.5	37.7	29	1	US-08-303-025-13
14	62.5	37.7	29	1	US-08-677-304-10
15	62.5	37.7	29	1	US-08-677-304-11
16	62.5	37.7	29	2	US-08-436-703B-15
17	62.5	37.7	29	2	US-08-436-703B-16
18	61	36.7	29	1	US-08-152-488-12
19	61	36.7	29	1	US-08-303-025-14
20	61	36.7	29	1	US-08-677-304-12
21	61	36.7	29	2	US-08-436-703B-16
22	57.5	34.6	28	1	US-08-303-025-12
23	57.5	34.6	28	2	US-08-436-703B-1
24	54.5	32.8	31	4	US-09-221-050-2
25	50	30.1	26	2	US-08-894-339-6
26	50	30.1	26	3	US-09-306-044-6
27	50	30.1	28	3	US-08-584-043A-22

28 50 30.1 29 3 US-08-584-043A-23 Sequence 23, Appl
29 50 30.1 30 3 US-08-584-043A-24 Sequence 24, Appl
30 50 30.1 31 3 US-08-584-043A-25 Sequence 25, Appl
31 50 30.1 32 3 US-08-584-043A-26 Sequence 26, Appl
32 50 30.1 33 3 US-08-584-043A-27 Sequence 27, Appl
33 50 30.1 33 3 US-08-584-043A-121 Sequence 121, Appl
34 50 30.1 34 3 US-08-584-043A-28 Sequence 28, Appl
35 50 30.1 34 3 US-08-584-043A-122 Sequence 122, Appl
36 50 30.1 35 3 US-08-584-043A-29 Sequence 29, Appl
37 50 30.1 35 3 US-08-584-043A-123 Sequence 123, Appl
38 49.5 29.8 31 3 US-08-995-172-2 Sequence 2, Appl
39 49.5 29.8 31 3 US-08-839-624-28 Sequence 28, Appl
40 49.5 29.8 31 3 US-09-150-812-28 Sequence 28, Appl
41 49.5 29.8 31 4 US-09-247-054-4 Sequence 4, Appl
42 49.5 29.8 32 1 US-08-231-730A-28 Sequence 28, Appl
43 49.5 29.8 32 1 US-08-427-001C-28 Sequence 28, Appl
44 49.5 29.8 32 1 US-08-457-798-28 Sequence 28, Appl
45 49.5 29.8 32 1 US-08-457-171-28 Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-09-405-743A-1
; Sequence 1, Application US/09405743A
; Patent No. 6514938
; GENERAL INFORMATION:
; APPLICANT: Yeda Research and Development Co., Ltd.
; TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
; FILE REFERENCE: 60807-A
; CURRENT APPLICATION NUMBER: US/09/405.743A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-405-743A-1

Query Match 100.0%; Score 166; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 3e-13;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AKKYAKKEKAAYKKEAKAARAAKAAAYEA 35
Db 1 AKKYAKKEKAAYKKEAKAARAAKAAAYEA 35

RESULT 2

US-09-816-989A-1
; Sequence 1, Application US/09816989A
; Patent No. 6800287
; GENERAL INFORMATION:
; APPLICANT: Lis, Doris
; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKERS
; FILE REFERENCE: 2609/60807-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/816.989A
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/101,693
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22402
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 35

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-1

Query Match 100.0%; Score 166; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 3e-13;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKKYAKKEKAAYKKEAKAKAAEAAAEAAEAA 35
Db 1 AKKYAKKEKAAYKKEAKAKAAEAAAEAAEAA 35

RESULT 3
US-08-152-488-13
; Sequence 13, Application US/08152488
; Patent No. 5534619
; GENERAL INFORMATION:
; APPLICANT: Wakefield, Thomas W.
; APPLICANT: Andrews, Philip C.
; APPLICANT: Stanley, James C.
; TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
; TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
; TITLE OF INVENTION: ANTICOAGULATION REVERSAL
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Benita J. Rohm, Esq.
; STREET: 512 Springfield Avenue
; CITY: Cranford
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07016-1811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 6; ASCII (DOS)Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/152,488
; FILING DATE: 12-NOV-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rohm, Benita J.
; REGISTRATION NUMBER: 28,664
; REFERENCE/DOCKET NUMBER: RM-7WG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-276-3344
; TELEFAX: 908-276-5543
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: N/A
; TOPOLOGY: N/A
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: N/A
; PUBLICATION INFORMATION:
; AUTHORS: N/A
; TITLE: N/A
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993

US-08-152-488-13
Query Match 40.7%; Score 67.5; DB 1; Length 32;
Best Local Similarity 61.3%; Pred. No. 0.1;
Matches 19; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

Qy 1 AKKYAKK-EKAAYKKEAKAKAAEAAAKE 30
Db 2 AKKAACKKAAYKKEAKAKAAEAAAKE 32

RESULT 4
US-08-303-025-15
; Sequence 15, Application US/08303025
; Patent No. 5614494
; GENERAL INFORMATION:
; APPLICANT: Wakefield, Thomas W.
; APPLICANT: Andrews, Philip C.
; APPLICANT: Stanley, James C.
; TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
; TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
; TITLE OF INVENTION: ANTICOAGULATION REVERSAL
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Benita J. Rohm, Esq.
; STREET: 150 West Jefferson, Suite 2500
; CITY: Detroit
; STATE: Michigan
; COUNTRY: United States of America
; ZIP: 48226-4415
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy diskette 3.5" 1.44Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS V.6.22
; SOFTWARE: Wordperfect 6.1; ASCII (DOS)Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/303,025
; FILING DATE: 08-SEPT-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06829
; FILING DATE: 14-AUG-1992
; APPLICATION NUMBER: US 08/152,488
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rohm, Benita J.
; REFERENCE/DOCKET NUMBER: 7WH-060548-00231
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 313-496-7622
; TELEFAX: 313-496-8454
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: N/A
; TOPOLOGY: N/A
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: N/A
; PUBLICATION INFORMATION:
; AUTHORS: N/A
; TITLE: N/A
; DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993

US-08-303-025-15
Query Match 40.7%; Score 67.5; DB 1; Length 32;
Best Local Similarity 61.3%; Pred. No. 0.1;
Matches 19; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

Qy 1 AKKYAKK-EKAAYKKEAKAKAAEAAAKE 30
Db 2 AKKAACKKAAYKKEAKAKAAEAAAKE 32

RESULT 5
US-08-677-304-13
; Sequence 13, Application US/08677304

Patent No. 5721212
GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
TITLE OF INVENTION: ANTICOAGULATION REVERSAL
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J. Rohm, Esq.
STREET: 512 Springfield Avenue
CITY: Cranford
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07016-1811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6; ASCII (DOS)Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,304
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/152,488
FILING DATE: 12-NOV-1993
APPLICATION NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
REGISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: RM-7MG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-276-3344
TELEFAX: 908-276-5543
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: No. 5721212 Relevant
TOPOLOGY: No. 5721212 Relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
TITLE: N/A
PUBLICATION INFORMATION:
DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
US-08-677-304-13

Query Match 40.7%; Score 67.5; DB 1; Length 32;
Best Local Similarity 61.3%; Pred. No. 0.1;
Matches 19; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

Qy 1 AKYAKK-EKAAKAYKKEAKAKAAEAAAKE 30
Db 2 AKKAAKAAKAAKAAKAAKAAKAAKAAK 32

RESULT 6
US-08-436-703B-2
Sequence 2, Application US/08436703B
Patent No. 5919761
GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR
TITLE OF INVENTION: HEPARIN AND LOW MOLECULAR

TITLE OF INVENTION: WEIGHT HEPARIN
TITLE OF INVENTION: ANTICOAGULATION REVERSAL
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J. Rohm, Esq.
STREET: 6601 Woodward Avenue
STREET: Suite 1525
CITY: Detroit
STATE: Michigan
COUNTRY: United States of America
ZIP: 48226
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk 1.44Mb, 3.5"
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6;
SOFTWARE: ASCII (DOS)Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,703B
FILING DATE: 08-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: N/A
FILING DATE: N/A
ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
REGISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: 7WK-060548-00233
TELECOMMUNICATION INFORMATION:
TELEPHONE: 313-965-1976
TELEFAX: 313-965-1951
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
TITLE: N/A
US-08-436-703B-2

Query Match 40.7%; Score 67.5; DB 2; Length 32;
Best Local Similarity 61.3%; Pred. No. 0.1;
Matches 19; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

Qy 1 AKYAKK-EKAAKAYKKEAKAKAAEAAAKE 30
Db 2 AKKAAKAAKAAKAAKAAKAAKAAKAAK 32

RESULT 7
US-08-303-025-16
Sequence 16, Application US/08303025
Patent No. 5614494
GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
TITLE OF INVENTION: ANTICOAGULATION REVERSAL
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J. Rohm, Esq.
STREET: 150 West Jefferson, Suite 2500
CITY: Detroit
STATE: Michigan
COUNTRY: United States of America
ZIP: 48226-4415


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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy diskette 3.5" 1.44Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS v.6.22
; SOFTWARE: WordPerfect 6.1; ASCII (DOS)Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/303,025
; FILING DATE: 08-SEPT-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06829
; FILING DATE: 14-AUG-1992
; APPLICATION NUMBER: US 08/152,488
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rohm, Benita J.
; REFERENCE/DOCKET NUMBER: 7WK-060548-00231
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 313-496-7622
; TELEFAX: 313-496-8454
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: N/A
; TOPOLOGY: N/A
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: N/A
; PUBLICATION INFORMATION:
; AUTHORS: N/A
; TITLE: N/A
; DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
; US-08-303-025-16

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Query Match 40.7%; Score 67.5; DB 1; Length 33;
Best Local Similarity 61.3%; Pred. No. 0.11;
Matches 19; Conservative 9; Mismatches 9; Indels 1; Gaps 1;

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Qy 1 AKYAKK-EKAAKAYKKEAKAAKAAAKE 30
Db 3 AKKAAKAAKAAKAAKAAKAAKAAKAAK 33

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RESULT 8
US-08-436-703B-4
; Sequence 4, Application US/08436703B
; Patent No. 5919761
; GENERAL INFORMATION:
; APPLICANT: Wakefield, Thomas W.
; APPLICANT: Andrews, Philip C.
; APPLICANT: Stanley, James C.
; TITLE OF INVENTION: NOVEL PEPTIDES FOR
; TITLE OF INVENTION: HEPARIN AND LOW MOLECULAR
; TITLE OF INVENTION: WEIGHT HEPARIN
; TITLE OF INVENTION: ANTICOAGULATION REVERSAL
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Benita J, Rohm, Esq.
; STREET: 6601 Woodward Avenue
; CITY: Detroit
; STATE: Michigan
; COUNTRY: United States of America
; ZIP: 48226
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk 1.44Mb, 3.5"
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6;
; SOFTWARE: ASCII (DOS)Text
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/436,703B
; FILING DATE: 08-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: N/A
; FILING DATE: N/A
; ATTORNEY/AGENT INFORMATION:
; NAME: Rohm, Benita J.
; REFERENCE/DOCKET NUMBER: 28,664
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 313-965-1976
; TELEFAX: 313-965-1951
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: N/A
; TOPOLOGY: N/A
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: N/A
; PUBLICATION INFORMATION:
; AUTHORS: N/A
; TITLE: N/A
; US-08-436-703B-4

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Query Match 40.7%; Score 67.5; DB 2; Length 33;
Best Local Similarity 61.3%; Pred. No. 0.11;
Matches 19; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

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Qy 1 AKYAKK-EKAAKAYKKEAKAAKAAAKE 30
Db 3 AKKAAKAAKAAKAAKAAKAAKAAKAAK 33

```

```

RESULT 9
US-08-152-488-10
; Sequence 10, Application US/08152488
; Patent No. 5534619
; GENERAL INFORMATION:
; APPLICANT: Wakefield, Thomas W.
; APPLICANT: Andrews, Philip C.
; APPLICANT: Stanley, James C.
; TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
; TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
; TITLE OF INVENTION: ANTICOAGULATION REVERSAL
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Benita J, Rohm, Esq.
; STREET: 512 Springfield Avenue
; CITY: Cranford
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07016-1811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6; ASCII (DOS)Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/152,488
; FILING DATE: 12-NOV-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rohm, Benita J.
; REFERENCE/DOCKET NUMBER: 28,664
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-276-3344

```


TELEFAX: 908-276-5543
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; STRANDEDNESS: N/A
; TOPOLOGY: N/A
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: N/A
; PUBLICATION INFORMATION:
; AUTHORS: N/A
; TITLE: N/A
; DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
US-08-152-488-10

Query Match 37.7%; Score 62.5; DB 1; Length 29;
Best Local Similarity 62.1%; Pred. No. 0.37;
Matches 18; Conservative 1; Mismatches 9; Indels 1; Gaps 1;
US-08-152-488-10

Qy 1 AKYAKKEKAAYKKEAKAKAEAAAK 29
Db 2 AKKAACKAKAKAKAKAKAKAKAKAK 29

RESULT 10
US-08-152-488-11
; Sequence 11, Application US/08152488
; Patent No. 5534619
; GENERAL INFORMATION:
; APPLICANT: Wakefield, Thomas W.
; APPLICANT: Andrews, Philip C.
; TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
; TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
; TITLE OF INVENTION: ANTICOAGULATION REVERSAL
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Benita J. Rohm, Esq.
; STREET: 512 Springfield Avenue
; CITY: Cranford
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07016-1811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6; ASCII (DOS)Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/152,488
; FILING DATE: 12-NOV-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rohm, Benita J.
; REGISTRATION NUMBER: 28,664
; REFERENCE/DOCKET NUMBER: RM-7WG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-276-3344
; TELEFAX: 908-276-5543
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; STRANDEDNESS: N/A
; TOPOLOGY: N/A
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:

; ORGANISM: N/A
; PUBLICATION INFORMATION:
; AUTHORS: N/A
; TITLE: N/A
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
US-08-152-488-11

Query Match 37.7%; Score 62.5; DB 1; Length 29;
Best Local Similarity 62.1%; Pred. No. 0.37;
Matches 18; Conservative 1; Mismatches 9; Indels 1; Gaps 1;
US-08-152-488-11

Qy 1 AKYAKKEKAAYKKEAKAKAEAAAK 29
Db 2 AKKAACKAKAKAKAKAKAKAKAKAK 29

RESULT 11
US-08-303-025-10
; Sequence 10, Application US/08303025
; Patent No. 5614494
; GENERAL INFORMATION:
; APPLICANT: Wakefield, Thomas W.
; APPLICANT: Andrews, Philip C.
; APPLICANT: Stanley, James C.
; TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
; TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
; TITLE OF INVENTION: ANTICOAGULATION REVERSAL
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Benita J. Rohm, Esq.
; STREET: 150 West Jefferson, Suite 2500
; CITY: Detroit
; STATE: Michigan
; COUNTRY: United States of America
; ZIP: 48226-4415
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy diskette 3.5" 1.44Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS v.6.22
; SOFTWARE: WordPerfect 6.1; ASCII (DOS)Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/303,025
; FILING DATE: 08-SEPT-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06829
; FILING DATE: 14-AUG-1992
; APPLICATION NUMBER: US 08/152,488
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rohm, Benita J.
; REFERENCE/DOCKET NUMBER: 7WH-060548-00231
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 313-496-7622
; TELEFAX: 313-496-8454
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; STRANDEDNESS: N/A
; TOPOLOGY: N/A
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: N/A
; PUBLICATION INFORMATION:
; AUTHORS: N/A
; TITLE: N/A
; DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
US-08-303-025-10


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; TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
; TITLE OF INVENTION: ANTICOAGULATION REVERSAL
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Benita J. Rohm, Esq.
; STREET: 512 Springfield Avenue
; CITY: Cranford
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07016-1811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6; ASCII (DOS)Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,304
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/152,488
; FILING DATE: 12-NOV-1993
; APPLICATION NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rohm, Benita J.
; REGISTRATION NUMBER: 28,664
; REFERENCE/DOCKET NUMBER: RM-7WG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-276-3344
; TELEFAX: 908-276-5543
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; STRANDEDNESS: No. 5721212 Relevant
; TOPOLOGY: No. 5721212 Relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: N/A
; PUBLICATION INFORMATION:
; AUTHORS: N/A
; TITLE: N/A
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
; US-08-677-304-10

Query Match 37.7%; Score 62.5; DB 1; Length 29;
Best Local Similarity 62.1%; Pred. No. 0.37;
Matches 18; Conservative 1; Mismatches 9; Indels 1; Gaps 1;

Qy 1 AKYAKKEKAAKAYKKEAKAAKAAK 29
Db 2 AKKAAKKAACKAAKKAACK-KAKKAACK 29

RESULT 15
US-08-677-304-11
; Sequence 11, Application US/08677304
; Patent No. 5721212
; GENERAL INFORMATION:
; APPLICANT: Wakefield, Thomas W.
; APPLICANT: Andrews, Philip C.
; APPLICANT: Stanley, James C.
; TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
; TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
; TITLE OF INVENTION: ANTICOAGULATION REVERSAL
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Benita J. Rohm, Esq.
; STREET: 512 Springfield Avenue
; CITY: Cranford

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; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07016-1811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6; ASCII (DOS)Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,304
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/152,488
; FILING DATE: 12-NOV-1993
; APPLICATION NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rohm, Benita J.
; REGISTRATION NUMBER: 28,664
; REFERENCE/DOCKET NUMBER: RM-7WG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-276-3344
; TELEFAX: 908-276-5543
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; STRANDEDNESS: No. 5721212 Relevant
; TOPOLOGY: No. 5721212 Relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: N/A
; PUBLICATION INFORMATION:
; AUTHORS: N/A
; TITLE: N/A
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
; US-08-677-304-11

Query Match 37.7%; Score 62.5; DB 1; Length 29;
Best Local Similarity 62.1%; Pred. No. 0.37;
Matches 18; Conservative 1; Mismatches 9; Indels 1; Gaps 1;

Qy 1 AKYAKKEKAAKAYKKEAKAAKAAK 29
Db 2 AKKAAKKAACKAAKKAACK-KAKKAACK 29

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Search completed: June 3, 2005, 10:01:19
Job time : 42 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2005, 10:09:37 ; Search time 38 Seconds
(without alignments)
113.941 Million cell updates/sec

Title: US-10-792-311-2
Perfect score: 213
Sequence: 1 AKYAKAKAKAKAKAYKAA.....AKYKAAAKAKAKAYKAA 45

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 293416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 10463

Minimum DB seq length: 0
Maximum DB seq length: 45

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	27.7	45	2 S10544	protamine phi-3.2
2	59	27.7	45	2 S04941	protamine phi-3.1
3	58	27.2	45	2 S10545	protamine phi-3.3
4	57	26.8	45	2 A05163	antifreeze protein
5	55.5	26.1	44	2 P10028	tandem repeat pept
6	49	23.0	32	2 A41270	protamine S4 - sma
7	48	22.5	33	2 A05162	antifreeze protein
8	48	22.5	40	2 S58853	homeotic protein u
9	46.5	21.8	40	1 PFI18G	antifreeze protein
10	45.5	21.4	39	2 S28908	dynamin-associated
11	43.5	20.4	35	2 A05112	M24 protein - Stre
12	42	19.7	33	1 PFI15G	antifreeze protein
13	41.5	19.5	36	2 F69800	hypothetical prote
14	41	19.2	37	1 FDFL3W	antifreeze protein
15	40	18.8	35	2 A24677	Balbani ring 2 ch
16	39.5	18.5	38	2 S23173	photosystem I chai
17	39.5	18.5	44	2 E99877	hypothetical prote
18	39	18.3	35	2 B24677	Balbani ring 2 ch
19	38.5	18.1	32	2 B40186	ubiquitin / riboso
20	38.5	18.1	35	2 B45316	sperm-specific pro
21	38.5	18.1	41	2 S10263	histone H3.2 - Tet
22	38	17.8	22	2 D47256	kinetoplast DNA-as
23	38	17.8	36	2 A34594	myosin regulatory
24	36.5	17.1	18	2 A61220	epsilon receptor m
25	36	16.9	42	2 A39124	nephritogenic prot
26	36	16.9	42	2 A47116	trifoliotoxin precu
27	35.5	16.7	44	2 T26815	hypothetical prote
28	35	16.4	20	2 S11416	ribosomal protein
29	35	16.4	41	2 S10267	histone H3.2 - Tet

30	35	16.4	41	2 S10283	histone H3.2 - Tet
31	35	16.4	41	2 S10289	histone H3.2 - Tet
32	35	16.4	41	2 S10287	histone H3.2 - Tet
33	35	16.4	41	2 S10291	histone H3.2 - Tet
34	35	16.4	41	2 S10295	histone H3.2 - Tet
35	35	16.4	41	2 S10297	histone H3.2 - Tet
36	35	16.4	41	2 S10299	histone H3.2 - Tet
37	35	16.4	41	2 S10285	histone H3.2 - Tet
38	35	16.4	41	2 S10259	histone H3.2 - Tet
39	35	16.4	41	2 S10261	histone H3.2 - Tet
40	35	16.4	41	2 S10265	histone H3.2 - Tet
41	35	16.4	41	2 S10269	histone H3.2 - Tet
42	35	16.4	41	2 S10271	histone H3.2 - Tet
43	35	16.4	41	2 S10273	histone H3.2 - Tet
44	35	16.4	41	2 S10275	histone H3.2 - Tet
45	35	16.4	41	2 S10277	histone H3.2 - Tet

ALIGNMENTS

RESULT 1

S10544
Protamine phi-3.2 - California mussel
N:Alternate names: protamine PL-IV.2
C:Species: Mytilus californianus (California mussel)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C:Accession: S10544
R:Ausio, J.; McParland, R.
Eur. J. Biochem. 182, 569-576, 1989
A:Title: Sequence and characterization of the sperm-specific protein phi3 from Mytilus ca
A:Reference number: S04941; MUID:89325302; PMID:2666130
A:Accession: S10544
A:Molecule type: protein
A:Residues: 1-45 <AUS>
A:Cross-references: UNIPROT:P11860
C:Superfamily: histone H1
C:Keywords: DNA binding; nucleus

Query Match 27.7%; Score 59; DB 2; Length 45;
Best Local Similarity 48.6%; Pred. No. 22;
Matches 17; Conservative 4; Mismatches 12; Indels 2; Gaps 1;

Qy 1 AKYAKAKAKAKAKAYKAAAKAKAYKAAK 35
Db 13 AVKSSKSKAKKPKSPKKKAAKPAK--KAAKKK 45

RESULT 2

S04941
Protamine phi-3.1 - California mussel
N:Alternate names: protamine PL-IV.1
C:Species: Mytilus californianus (California mussel)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C:Accession: S04941
R:Ausio, J.; McParland, R.
Eur. J. Biochem. 182, 569-576, 1989
A:Title: Sequence and characterization of the sperm-specific protein phi3 from Mytilus ca
A:Reference number: S04941; MUID:89325302; PMID:2666130
A:Accession: S04941
A:Molecule type: protein
A:Residues: 1-45 <AUS>
A:Cross-references: UNIPROT:P11860
A:Note: 6-Thr, 17-Thr, and 18-Thr was also found
C:Superfamily: histone H1
C:Keywords: DNA binding; nucleus

Query Match 27.7%; Score 59; DB 2; Length 45;
Best Local Similarity 48.6%; Pred. No. 22;
Matches 17; Conservative 4; Mismatches 12; Indels 2; Gaps 1;

Qy 1 AKYAKAKAKAKAKAYKAAAKAKAYKAAK 35
Db 13 AVKSSKSKAKKPKSPKKKAAKPAK--KAAKKK 45

13 AVKSSSKAKPKSPKKKAAPAK--KAAKK 45

RESULT 3

protamine phi-3.3 - California mussel
N/Alternate names: protamine PL-IV.3
C/Species: Mytilus californianus (California mussel)
C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #
C/Accession: S10545

R;Ausio, J.; McParland, R.
Eur. J. Biochem. 182, 569-576, 1989
A;Title: Sequence and characterization of the sperm-specific protein phi3 from *Mytilus*
A;Reference number: S04941; PMID:89325302; PMID:2666130
A;Accession: S10545
A;Molecule type: protein
A;Residues: 1-45 <AUS>
A;Cross-references: UNIPROT:P11860
C;Superfamily: histone H1
C;Keywords: DNA binding; nucleus

Query Match	27.2%	Score 58;	DB 2;	Length 45;
Best Local Similarity	36.6%	Pred. No. 27;		
Matches	15;	Conservative	8;	Mismatches 18;
Indels	0;	Gaps	0;	

QY	5	AKKAKAEKAKAYKAAEAKKAAKYEKAAAEKAAAEKAAEYEA	45
		:: : : : : : : :	
Dp	1	AKAKRSPPKKKAAAVKSSKSKAKKPKSPKKKKAAKKPKARKA	41

RESULT 4

A03163
anifreeze protein SS-8 - shorthorn sculpin
C/Species: Myoxocephalus scorpius (shorthorn sculpin, daddy sculpin)
C/date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C/accession: A03163
R/hew, C.L.; Joshi, S.; Wang, N.C.; Kao, M.H.; Ananthanarayanan, V.S.
Eur. J. Biochem. 151, 167-172, 1985
A/Title: Structures of shorthorn sculpin anifreeze polypeptides.
A/Reference number: A91150; MUID:85285003; PMID:4029130

A:Accession: A05163
A:Molecule type: protein
A:Residues: 1-45 <HEM>
A:Cross-references: UNIPROT:P04368
C:Superfamily: antifreeze protein
C:Keywords: antifreeze; blocked amino
P:9.45/Region: alanine-rich
F:1/Modified site: blocked amino end (Met) #status experimental

Query Match	26.8%	Score 57;	DB 2;	Length 45;
Best Local Similarity	56.2%	Pred. No. 34;		
Matches	18:	Conservative	0:	Mismatches
			14:	Indels
				Gaps

Qy 14 KKAYKAAEAKKAAYEKAAAEKAAAKEAAYEA 45
| | | | | | | | | | | | | | | |
Dp 9 KAARIABAAAAT.AAKTAADAPAAAKAAAKAATAA 40
| | | | | | | | | | | | | | | |

RESIST 5

RES001 5
 PT0028
 tandem repeat peptide chain - Leishmania major (clone 39) (fragment)
 C:Species: Leishmania major
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
 C:Accession: PT0028
 R:Wallis, A.E.; McMaster, W.R.
 J. Exp. Med. 166, 1814-1824, 1987
 A:Title: Identification of Leishmania genes encoding proteins containing tandemly repeated
 A:Reference number: PT0027. PMID:88061089. PMID:3502718

A;Accession: F10028
A;Molecule type: mRNA
A;Residues: 1-44 <WAS>
A;Cross-references: UNIPROT:P14700; EMBL:X06556
A;Experimental source: strain NIH S

Query Match 26.1%; Score 55.5; DB 2; Length 44;
Best Local Similarity 40.0%; Pred. No. 46;
Matches 16: Conservative 10; Mismatches 13; Indels

QY 5 AKKAKAEKAYKAAEAKKAAYEKAAAEKAAKEAAE 44
| : || : | : || : || : | : || : | :
Db 5 AARLOAEFAAARCOAEFEAAARLO-AEAEEAARLOAEAE 43

RESULT 6

K05001 6
 A12170
 protamine S4 - smaller spotted catshark
 N; Alternate names: scyllorhinine S4
 C; Species: Scyllorhinus canicula (smaller spotted dogfish)
 C; Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 09-Jul-2004
 C; Accession: A41270; S12285
 R; Sautiere, P.; Gusew, M.; Briand, G.; Martinage, A.; Chevaillier, P.
 Biochim. Biophys. Acta 791, 82-85, 1984
 A; title: Primary structure of scyllorhinine S4, a protamine isolated from sperm nuclei
 A; Reference number: A41270
 A; Accession: A41270
 A; Status: preliminary
 A; Molecule type: protein
 A; Residues: 1-32 <SAU>
 A; Cross-references: UNIPROT:P30259
 R; Gusew, M.; Sautiere, P.; Chauviere, M.; Chevaillier, P.
 Biochim. Biophys. Acta 740, 93-98, 1983
 A; title: Extraction, purification and characterization of the sperm protamines of the dogfish
 A; Reference number: S01463; MUID:84000513; PMID:6615852
 A; Accession: S12285
 A; Molecule type: protein
 A; Residues: 1-5 <GUS>
 C; Keywords: DNA binding; sperm; testis

Query Match 23.0%; Score 49; DB 2; Length 32;
Best Local Similarity 41.4%; Pred. No. 1.4e+02;
Matches 12: Conservative 3; Mismatches 14; Indels

QY	12	KAKKAYKAAEAKCAAKYKAAAEKAAAKE	40
		: :	
dh	3	KCKKARKCPCKCKKARKCPCKCKRKVAKCK	31

RESULT 7

antifreeze protein SS-3 - shorthorn sculpin
C/Species: Myoxocephalus scorpius (shorthorn sculpin, daddy sculpin)
C/Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C/Accession: A05162
R/Hew, C.L.B.; Joshi, S.; Wang, N.C.; Kao, M.H.; Ananthanarayanan, V.S.
Eur. J. Biochem. 151, 167-172, 1985
A/Ritle: Structures of shorthorn sculpin antifreeze polypeptides.
A/Reference number: A91150; MUID:85285003; PMID:4029130
A/Accession: A05162
A/Molecule type: protein
A/Residues: 1-33 <HEW>
A/Cross-references: UNIPROT:P04367
C/Superfamily: antifreeze protein
C/Keywords: antifreeze

Query Match 22.5%; Score 48; DB 2; Length 33;
Best Local Similarity 51.4%; Pred. No. 1.8e+02;
Matches 18: Conservative 2; Mismatches 11; Indels

Q7 8 AKAEKAKKAYKAAEAKCAKYEKAAEAKKAAKAA 42
| | | | | | | | | | | | | | | | | | | | | |
D6 3 APARAAAKT--AADALAAAK--KTAADAAAAA 33
| | | | | | | | | | | | | | | | | | | | | |

RESULT 8

RESULTS
S50853
homeotic protein ultrabithorax homolog - Junonia coenia (fragment)


```

DB      DB      ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|||||
2 AKKAKEALEAKERYMEEMADTADAIEATLDEKMAEE 38

RESULT 11
A05112
M24 protein - Streptococcus pyogenes (fragment)
C:Species: Streptococcus pyogenes
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C:Accession: A05112
R:Beachey, E.H.; Seyer, J.M.; Dale, J.B.; Hasty, D.L.
J. Biol. Chem. 258, 13250-13257, 1983
A:Reference number: A05112; MUID:84032558; PMID:6415061
A:Accession: A05112
A:Molecule type: protein
A:Residues: 1-35 <BEA>
A:Cross-references: UNIPROT.Q7W1B4
C:Superfamily: M5 protein

Query Match          20.4%; Score 43.5; DB 2; Length 35;
Best Local Similarity 53.6%; Pred. No. 4.9e+02;
Matches 15; Conservative 3; Mismatches 7; Indels 3; Gaps 2;

QY      QY      ||:||:||:||:||:||:||:||:||:||:|||||
10 AEKAKYKAAEAKKAA-KYEKAAAEKA 36
DB      DB      ||:||:||:||:||:||:||:||:||:|||||
5 ADSAK-IKTLEAKAEAKADLEKA 30

RESULT 12
FDI5G
antifreeze protein GS-5 - grubby sculpin
C:Species: Myoxocephalus aeneus (grubby sculpin)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C:Accession: S06417
R:Chakrabarty, A.; Hew, C.L.; Shears, M.; Fletcher, G.
Can. J. Zool. 66, 403-408, 1988
A>Title: Primary structures of the alanine-rich antifreeze polypeptides from grubby sculpin
A:Reference number: S06417
A:Accession: S06417
A:Molecule type: protein
A:Residues: 1-33 <CHA>
A:Cross-references: UNIPROT.P20421
C:Superfamily: antifreeze protein
C:Keywords: antifreeze; blocked amino end
F/I/Modified site: blocked amino end (Met) #status experimental

Query Match          19.7%; Score 42; DB 1; Length 33;
Best Local Similarity 54.2%; Pred. No. 6.4e+02;
Matches 13; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY      QY      ||:||:||:||:||:||:||:||:|||||
16 AYKAAEKAAKYEAKEAAAEKAAAK 39
DB      DB      ||:||:||:||:||:||:||:|||||
9 AKTAADALAAKKTTADAAAAAAK 32

RESULT 13
F69800
hypothetical protein yfhe - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: F69800
R:Kunet, P.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berterio, L.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, A.A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabref, C.; Ferrari, E.; Nature 390, 249-256, 1997
A:Authors: Fulgider, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallert, I.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Kletter, P.; Koningsberg, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidos, A.; Lardinois, A.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, A.; Authors: Schlögl, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, Akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

```


Qy 9 KAEKAKKAYKAAEAKKAAK 27
db 1 KPEKCGSAMKRTAEAKCAR 19

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OM protein - protein search, using sw model

Run on: June 3, 2005, 10:01:26 ; Search time 171 Seconds
(without alignments)
134.758 Million cell updates/sec

Title: US-10-792-311-2

Perfect score: 213

Sequence: 1 AKYAKAKAEKAKKAYKAA.....AKYKAAAEKAAKAAAYEA 45

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 57864

Minimum DB seq length: 0

Maximum DB seq length: 45

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	33.8	44	2 Q711Y2	Q711Y2 lactobacilli
2	70.5	33.1	43	2 Q6MGW9	Q6MGW9 Bdellovibrio
3	68	31.9	35	2 Q747M3	Q747M3 geobacter s
4	63.5	29.8	42	2 Q9DF18	Q9DF18 myoxocephal
5	59	27.7	45	1 PH13 MYTCA	P11860 mytilus cal
6	57	26.8	45	1 ANP8 MYOSC	P04368 myoxocephal
7	49	23.0	32	1 PRT4_SCYCA	P30259 scyllorhinu
8	48	22.5	33	1 ANP3 MYOSC	P04367 myoxocephal
9	48	22.5	42	2 Q25210	Q25210 junonia coe
10	47	22.1	42	2 Q96RT9	Q96RT9 homo sapien
11	46.5	21.8	40	1 ANP8 MYOAE	P20617 myoxocephal
12	45.5	21.4	39	2 Q9QW40	Q9QW40 rattus sp.
13	45	21.1	44	2 Q818F4	Q818F4 bacillus ce
14	45	21.1	44	2 Q82G43	Q82G43 streptomyce
15	44.5	20.9	37	2 Q85035	Q85035 mycoplasma
16	44	20.7	37	2 Q74CW2	Q74CW2 geobacter s
17	44	20.7	40	2 Q8EJK5	Q8EJK5 shewanella
18	44	20.7	44	2 Q73AA3	Q73AA3 bacillus ce
19	44	20.7	44	2 Q81S66	Q81S66 bacillus an
20	43.5	20.4	35	2 Q7M1B4	Q7M1B4 streptococc
21	43.5	20.4	35	2 Q83175	Q83175 cauliflowe
22	43.5	20.4	38	2 Q7S1C4	Q7S1C4 pseudopleur
23	43	20.2	39	2 Q86N15	Q86N15 caenorhabdi
24	43	20.2	42	2 Q7RH04	Q7RH04 plasmodium
25	42	19.7	33	1 ANP5 MYOAE	P20421 myoxocephal
26	42	19.7	35	2 Q65RE2	Q65RE2 mammeimia
27	41.5	19.5	36	1 YFHE BACSU	Q81573 bacillus su
28	41.5	19.5	43	2 Q8LFC5	Q8LFC5 arabidopsis
29	41	19.2	22	2 Q7JQ96	Q7JQ96 psammechinu
30	41	19.2	37	1 ANP3_PSEAM	P02733 pseudopleur
31	40	18.8	32	2 Q8P3B2	Q8P3B2 xanthomonas

32 40 18.8 32 2 Q8PEL7 Q8pel7 xanthomonas
33 40 18.8 38 2 Q7RA66 Q7ra66 plasmodium
34 40 18.8 38 2 Q9S9D9 Q9s9d9 nicotiana t
35 40 18.8 41 2 Q7REB3 Q7reb3 plasmodium
36 40 18.8 42 2 Q8EK33 Q8ek33 shewanella
37 39.5 18.5 44 2 Q99V18 Q99v18 staphylococ
38 39.5 18.5 44 2 Q7A176 Q7a176 staphylococ
39 39.5 18.5 44 2 Q7A690 Q7a690 staphylococ
40 39.5 18.5 44 2 Q6GAD5 Q6gad5 staphylococ
41 39.5 18.5 44 2 Q6GI06 Q6gi06 staphylococ
42 39 18.3 36 2 Q62601 Q62601 colpidium c
43 39 18.3 38 2 Q9UAS9 Q9uas9 boophilus m
44 39 18.3 41 2 Q6J7X0 Q6j7x0 actinoplane
45 39 18.3 41 2 Q84W05 Q84w05 arabidopsis

ALIGNMENTS

RESULT 1

Q711Y2 PRELIMINARY; PRT; 44 AA.
AC Q711Y2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Histone-like protein (Fragment).
OS Lactobacillus delbrueckii (subsp. lactis).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=29397;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 4797;
RA Langenheim J.F., Ulrich R.L.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF496145; AAQ06805.1; --
FT NON_TER 1 1
FT NON_TER 44 44
SQ SEQUENCE 44 AA; 4634 MW; CAC365D7CFC6A162 CRC64;

Query Match 33.8%; Score 72; DB 2; Length 44;
Best Local Similarity 48.6%; Pred. No. 3.6;
Matches 18; Conservative 4; Mismatches 15; Indels 0; Gaps 0;

Qy 3 KYAKKAKAEKAKAYKAAEAKKAAKAEKAAEAKAAK 39

Db 1 KSTTKAAKSAKSTTKAAKSAKSTTKAAKSAKSTTKAAKSAK 37

RESULT 2

Q6MGW9 PRELIMINARY; PRT; 43 AA.
AC Q6MGW9;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusName=Bd3800;
OS Bdellovibrio bacteriovorus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
OC Bdellovibrionaceae; Bdellovibrio.
OX NCBI_TaxID=959;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
RX PubMed=14752164; DOI=10.1126/science.1093027;
RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
Keller H., Lambert C., Evans K.J., Goemann A., Meyer F.,
RA Sockett R.E., Schuster S.C.;
RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
genomic perspective.";
RL Science 303:689-692(2004).


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DR  EMBL; BX842656; CAE81160.1; -.
SQ  Complete proteome.
KW  SEQUENCE 43 AA; 4598 MW; 11AB9E05A80493C CRC64;

Query Match      33.1%; Score 70.5; DB 2; Length 43;
Best Local Similarity 50.0%; Pred. No. 4.9;
Matches 21; Conservative 2; Mismatches 18; Indels 1; Gaps 0

QY  1 AKKYAKKAAKAEKAKYKAAEAKKAAKYKAAAEKAAAEKAA 42
    ||||| : ||| |||||
DB  2 AKKAAKATKKA VKVTKTKV-AKKATKKVAKKATKKATKKA 42
    ||||| : ||| |||||

RESULT 3
Q747M3 PRELIMINARY; PRT; 35 AA.
ID AC Q747M3
DC Q747M3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE DE Hypothetical protein.
GN O:deredLocuNames=GSU3242;
OS Geobacter sulfurreducens.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OC Geobacteraceae; Geobacter.
OX NCBI_TaxID=35554;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCA / ATCC 51573;
RX PubMed=14671304; DOI=10.1126/science.1088727;
RA Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
RA Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,
RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
RA Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
RA Davidson T.M., Zafar N., White O., Tran B., Romero C., Forberger H.,
RA Weidman J.F., Khouri H.M., Feldblyum T.V., Utterback T.R.,
RA Van Aken S.E., Lovley D.R., Fraser C.M.;
RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
RT environments.";
RL Science 302:1967-1969 (2003).
DR EMBL; AE017180; AAR36633.1; -.
DR TIGR; GSU3242; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 35 AA; 3966 MW; 0E6E2B600A034777 CRC64;

Query Match      31.9%; Score 68; DB 2; Length 35;
Best Local Similarity 50.0%; Pred. No. 7.1;
Matches 17; Conservative 4; Mismatches 13; Indels 0; Gaps 0

QY  6 KKAKAEKAKKAYKAAEAKKAAKYKAAAEKAAAEKAAK 39
    ||| : ||| |||||
DB  2 KKEEKPVKKAKKAKKAKKEEKEEAAAPAEKK 35
    ||| : ||| |||||

RESULT 4
Q9DF18 PRELIMINARY; PRT; 42 AA.
ID AC Q9DF18
DC Q9DF18;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE DE Longhorn sculpin skin-type antifreeze protein.
OS Myxoxocephalus octodecimspinosus (Longhorn sculpin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Acanthopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Neopterygii; Percormorpha; Ruteleostei; Neoteleostei;
OC Cottoidae; Cottidae; Myxoxocephalus.
OX NCBI_TaxID=68557;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=21132197; PubMed=11136728; DOI=10.1074/jbc.M009293200;
RA Low W.-K., Lin Q., Stathakis C., Miao M., Fletcher G.L., Hew C.L.;

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[illegible]


```

Query Match      22.5%; Score 48; DB 1; Length 33;
Best Local Similarity 51.4%; Pred. NO. 5.9e+02;
Matches 18; Conservative 2; Mismatches 11; Indels 4; Gap

```

QY 8 AKAEKAKAYKAAAEAKKAAKYEKAAAEKAAAEKAA 42
 DB 3 APAPAAAKT--AADAALAAK--KTAADAAAAA 33

```

RESULT 9
Q25210 PRELIMINARY; PRT; 42 AA..
AC Q25210;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Untrabithorax homeodomain protein (Fragment).
OS Junonia coenia (Peacock butterfly) (Precis coenia).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Papilionoidea; Nymphalidae; Nymphalinae; Junonia.
ON NCBI_TaxID=39708;
RX [1]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=95075456; PubMed=7840822; DOI=10.1038/372458a0;
RA Warren R.W., Nagy L., Selegue J., Gates J., Carroll S.;
RT "Evolution of homeotic gene regulation and function in flies and
RT butterflies.;"
RL Nature 372:458-461(1994).
DR EMBL; L42137; AA868463.1; -.
DR PIR; S58853; S58853.
DR GO; GO:0005634; C:nucleus; IEA.
KW Nuclear protein.
FT NON TER 1
FT FT 1
SQ SEQUENCE 42 AA; 4380 MW; 53C002E55430FE32 CRC64;

```

```

Query Match      22.5%; Score 48; DB 2; Length 42;
Best Local Similarity 50.0%; Pred. NO. 7.4e+02;
Matches 12; Conservative 4; Mismatches 8; Indels 0; Gap

```


Q82G43	Q82G43	PRELIMINARY;	PRT;	44 AA.
ID	Q82G43			
AC	Q82G43;			
DT	01-JUN-2003 (TrEMBLrel. 24, Created)			
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)			
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)			
DE	Hypothetical protein.			
DE	Hypothetical protein.			
GN	OrderedLocusNames=SAV4055;			
OS	Streptomyces avermitilis.			
OS	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;			
OC	Streptomycineae; Streptomycetaceae; Streptomyces.			
OC	NCBI_TaxID=33903;			
OX	[1]			
RN	SEQUENCE FROM N.A.			
RP	STRAIN=MA-4680;			
RC	MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;			
RX	Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,			
RA	Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonce T.,			
RA	Kikuchi H., Shiba T., Sakaki Y., Hattori M.;			
RA	"Genome sequence of an industrial microorganism Streptomyces			
RT	avermitilis: deducing the ability of producing secondary			
RT	metabolites.";			
RT	Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).			
RL	[2]			
RL	SEQUENCE FROM N.A.			
RP	STRAIN=MA-4680;			
RC	MEDLINE=22608306; PubMed=12692562;			
RX	Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,			
RA	Sakaki Y., Hattori M., Omura S.;			
RA	"Complete genome sequence and comparative analysis of the industrial			
RT	microorganism Streptomyces avermitilis.";			
RT	Nat. Biotechnol. 21:526-531(2003).			
RL	EMBL; AP005037; BAC71767.1; -.			
DR	Complete proteome; Hypothetical protein.			
KW	SEQUENCE 44 AA; 4867 MW; 435C4EB1EBF3A577 CRC64;			
SQ				
Query Match 21.1%; Score 45; DB 2; Length 44;				
Best Local Similarity 39.3%; Pred. No. 1.5e+03;				
Matches 11; Conservative 6; Mismatches 11; Indels 0; Gaps 0;				
QY	4 YAKCAKAEKAKAYKAAEAKKAAKYEKA 31			
DB	3 FHKVAPVKPKRKAAPAAAPAKKAQHKPA 30			
	:			
	:			
RESULT 15				
O85035	PRELIMINARY;	PRT;	37 AA.	
ID	O85035			
AC	O85035;			
DT	01-NOV-1998 (TrEMBLrel. 08, Created)			
DT	01-NOV-1998 (TrEMBLrel. 08, Last sequence update)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE	Hypothetical protein.			
DE	Hypothetical protein.			
OS	Mycoplasma hominis			
OC	Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.			
OC	NCBI_TaxID=2098;			
OX	[1]			
RN	SEQUENCE FROM N.A.			
RP	STRAIN=PG21;			
RC	MEDLINE=98353329; PubMed=9687401;			
RX	Bebear C.M., Charron A., Bove J.M., Bebear C., Renaudin J.;			
RA	"Cloning and nucleotide sequences of the topoisomerase IV parC and			
RT	parE genes of Mycoplasma hominis.";			
RT	Antimicrob. Agents Chemother. 42:2024-2031(1998).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RP	STRAIN=PG21;			
RC	MEDLINE=98353329; PubMed=9687401;			
RX	Bebear C.M., Charron A., Bove J.M., Bebear C., Renaudin J.;			
RA	submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.			
RL	EMBL: AF031691; AAC33843.1; -.			
DR	EMBL: AF031691; AAC33843.1; -.			

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OM protein - protein search, using sw model

Run on: June 3, 2005, 10:00:36 ; Search time 157 Seconds

(without alignments)
110.855 Million cell updates/sec

Title: US-10-792-311-2

Perfect score: 213

Sequence: 1 AKYAKAKAKAKAKAYAA.....AKYKAAKAAKAAKAAKAYEA 45

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 913638

Minimum DB seq length: 0

Maximum DB seq length: 45

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04.*

1: Geneseq1980s.*

2: Geneseq1990s.*

3: Geneseq2000s.*

4: Geneseq2001s.*

5: Geneseq2002s.*

6: Geneseq2003as.*

7: Geneseq2003bs.*

8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	213	100.0	45	3	AY82572	Copolymer
2	108	50.7	35	3	AY82571	Copolymer
3	86	40.4	39	2	AAW44934	Mycobacte
4	86	40.4	39	7	ADF45561	Methylate
5	74.5	35.0	32	2	AAR90180	Polycatio
6	74.5	35.0	32	2	AAW06686	Protamine
7	74.5	35.0	33	2	AAR90181	Polycatio
8	74.5	35.0	33	2	AAW06688	Protamine
9	74	34.7	40	3	AAR08170	Peptide m
10	72	33.8	29	2	AAR90178	Polycatio
11	72	33.8	29	2	AAR90176	Polycatio
12	72	33.8	29	2	AAW06687	Protamine
13	72	33.8	29	2	AAW06697	Protamine
14	69	32.4	32	3	AAW08175	Peptide m
15	68	31.9	36	3	AAW08169	Peptide m
16	67	31.5	28	2	AAR90177	Polycatio
17	67	31.5	28	2	AAW06685	Protamine
18	67	31.5	38	2	AAW22872	P. americ
19	66.5	31.2	42	8	AD043175	Peptide u
20	66	31.0	29	2	AAR90179	Polycatio
21	66	31.0	29	2	AAW06698	Protamine
22	64	30.0	38	2	AAW22868	P. americ
23	64	30.0	38	3	AAV44714	Winter fl
24	63.5	29.8	32	3	AAW08168	Peptide m
25	63	29.6	42	4	AAO09072	Human pol

26	62.5	29.3	37	2	AAW08398	Nucleic a
27	62.5	29.3	37	2	AAW08396	Nucleic a
28	62.5	29.3	37	2	AAW38228	NBC9 pept
29	62.5	29.3	37	2	AAW52875	Nucleic a
30	62.5	29.3	38	2	AAW65937	Histone b
31	62.5	29.3	38	2	AAW69208	Nucleic a
32	62	29.1	45	2	AAW24450	Nucleic a
33	62	29.1	45	3	AY98493	Peptide #
34	62	29.1	45	3	AY59038	Peptide u
35	62	29.1	45	4	AAW45846	Nucleic a
36	62	29.1	45	4	AAU04283	Trimeric
37	61	28.6	39	2	AAW22881	P. americ
38	61	28.6	39	2	AAW22876	Synthetic
39	60.5	28.4	30	3	AAW08167	Peptide m
40	60	28.2	28	8	AD043177	Peptide u
41	60	28.2	28	8	AD043181	NBC11 pep
42	59.5	27.9	31	2	AAW38224	Adn11701
43	59.5	27.9	31	8	ADN11701	Peptide l
44	59	27.7	38	2	AAW38892	Delivery
45	59	27.7	39	2	AAW38893	Delivery

ALIGNMENTS

RESULT 1

AY82572

ID AY82572 standard; peptide; 45 AA.

XX

AC AY82572;

XX

DT 28-JUL-2000 (first entry)

XX

DE

XX

XX

XX

KW

KW

KW

KW

KW

KW

KW

KW

XX

OS Unidentified.

XX

PN WO200018794-A1.

XX

PD 06-APR-2000.

XX

PF 24-SEP-1999; 95WO-US022402.

XX

PR 25-SEP-1998; 98US-0101693P.

XX

PA (YEDA) YEDA RES & DEV CO LTD.

XX

PI (TEVA-) TEVA PHARM USA INC.

XX

PI Gad A, Lis D;

XX

DR WPI; 2000-317499/27.

XX

PT Copolymer 1 related polypeptides used as molecular weight markers for

XX

PS Claim 10; Page 14; 72pp; English.

XX

XX

CC

CC

CC

CC

CC

CC

CC

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:2.

Copolymer; molecular weight marker; TV-marker; immune disease;
glutramer acetate; autoimmune disease; antiarthritic; neuroprotective;
osteopathic; immunosuppressive; antithyroid; antiinflammatory;
antidiabetic; thyromimetic; haemostatic; antiporiatic; dermatological;
antianemic; immunosuppressive; demyelinating disease; osteoarthritis;
inflammatory condition; multiple sclerosis; rheumatoid arthritis;
Crohn's disease; chronic immune thrombocytopaenia purpura; colitis;
diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis;
Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
pemphigus vulgaris; systemic lupus erythematosus.

Unidentified.

WO200018794-A1.

06-APR-2000.

24-SEP-1999; 95WO-US022402.

25-SEP-1998; 98US-0101693P.

(YEDA) YEDA RES & DEV CO LTD.

(TEVA-) TEVA PHARM USA INC.

Gad A, Lis D;

WPI; 2000-317499/27.

Copolymer 1 related polypeptides used as molecular weight markers for
glutramer acetate and for treatment and prevention of immune diseases.

Claim 10; Page 14; 72pp; English.

AY82571 to AY82577 represent specifically claimed copolymer molecular
weight TV-marker polypeptides from the present invention. The present
invention describes polypeptides (I) for determining the molecular weight
of a copolymer (CP), which has an identified molecular weight and an
amino acid composition corresponding to the copolymer. The polypeptides

of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune ophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, Crohn's disease, chronic immune thrombocytopenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers

```
Query Match      100.0%; Score 213; DB 3; Length 45;
Best Local Similarity 100.0%; Pred. NO. 3.4e-16;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

RESULT 2	
AAAY82571	
ID	AAAY82571 standard; peptide; 35 AA.
XX	
XX	AAAY82571;
XX	
XX	28-JUL-2000 (first entry)
XX	
DE	Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:1.
XX	
XX	Copolymer: molecular weight marker: TV-marker: immune disease;
KW	glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective
KW	osceopathic; immunosuppressive; antithyroid; antiinflammatory;
KW	antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatologica
KW	antianemic; immunosuppressive; demyelinating disease; osteoarthritis
KW	inflammatory condition; multiple sclerosis; rheumatoid arthritis;
KW	Crohn's disease; chronic immune thrombocytopaenia purpura; colitis;
KW	diabetes mellitus; Graves disease; Gullain-Barre's syndrome; psoriasis
KW	Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
KW	hemiphagic vulgaris; systemic lupus erythematosus.

XX	Unidentified.	
OS		
XX	WO200018794-A1.	
XX		
PN		
XX	06-APR-2000.	
XX		
PD		
XX		
XX	24-SEP-1999; 99WO-US022402.	
PF		
XX		
XX	25-SEP-1998; 98US-0101693P.	
PR		
XX	(YEDA) YEDA RES & DEV CO LTD.	
PA	(TEVA-) TEVA PHARM USA INC.	
PA		
XX		
PI	Gad A, Lis D;	
XX		
XX		
DR	WPI; 2000-317499/27.	
XX		
XX		
PT	Copolymer 1 related polypeptides used as molecular weight markers for	
PT	glatiramer acetate and for treatment and prevention of immune diseases.	
XX		
XX	Claim 10; Page 14; 72pp; English.	
PS		

AA82571 to AA82577 represent specifically claimed copolymer molecular

weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for Glatramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune ophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, Crohn's disease, chronic immune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated diseases which can be treated include host-versus-graft disease, grafted-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to Glatramer acetate molecules, which makes them ideal for use as molecular weight markers

Query Match	50.7%	Score 108;	DB 3;	Length 35;
Best Local Similarity	64.4%	Pred. No. 6.8e-05;		
Matches 29; Conservative	1;	Mismatches 5;	Indels 10;	Gaps 2

QY 1 AKYAKKAEKAKKAYKAAEAKKAYEKAAAEKAAAEKAAEYEA 45
||||| || ||||| | || : ||||| |||||
Db 1 AKYAKKEA--AKKAYK-----KEAKAAEAAAEKAAEYEA 35

RESULT 3
AAW44934
ID AAW44934 standard; peptide; 39 AA.

XX
DT 14-OCT-1998 (first entry)
XX
DE Mycobacterial heparin-binding haemagglutinin antigen peptide fragment

Surface protein; *Mycobacterium bovis*; BCG; adhesion; epithelium;
KW Bacille Calmette-Guérin; *Mycobacterium tuberculosis*; epithelial cell;
KW Heparin-binding haemagglutinin antigen; PCR; primer; amplification;
KW probe; hybridisation; chromosome; vaccine; diagnosis; immunosay.

OS *Mycobacterium bovis*.

PN WO9744463-A2.

27-NOV-1997.

20-MAY-1997:

PR 17-MAY-1996: 96FR-00006168.

XX PA (TNSP) TNST PASTEUR I.I.I.I.E.

PA (INRM) INST NAT SANTE & RECH MEDICALE:
XX

PI Menozzi F, Locher C;
yy

DR WPI; 1998-018517/02.

PT New peptide(s) involved in adhesion of mycobacteria to epithelial cells
PT
PT used in vaccines and for diagnosing mycobacterial infection, also use of
PT sulphated saccharide(s) and glyco-conjugate(s) to prevent mycobacterial
PT adhesion.
PT

XX PS Claim 5; Page 35; 52pp; French.

CC This peptide represents a fragment of a surface protein found on

CC Mycobacterium bovis BCG (Bacille Calmette-Guerin) or M. tuberculosis,
 CC which enable mycobacteria to adhere to host, especially epithelial,
 CC cells. The antigen was isolated by passing a culture of BCG
 CC microorganisms over a Heparin-Sepharose column and eluting proteins with
 CC a gradient of 0-0.5 M NaCl. Fractions were separated by gel
 CC electrophoresis and a 28 kD heparin binding protein purified. N-terminal
 CC and internal peptide fractions were sequenced and the amino acid
 CC sequences used to design PCR primers. These amplified a 150 bp fragment
 CC (AAT76947) used as a probe to isolate chromosomal fragments containing
 CC the gene (AAT76948). The gene encodes a protein which is a heparin-
 CC binding haemagglutinin antigen (HBHA). The peptide can be used in
 CC vaccines against mycobacterial infections (particularly M. bovis or M.
 CC tuberculosis), or can be used to diagnose mycobacterial infection (by
 CC immunoassay detection of anti-HBHA antibodies)
 XX
 SQ Sequence 39 AA;

Query Match 40.4%; Score 86; DB 2; Length 39;
 Best Local Similarity 65.6%; Pred. No. 0.019;
 Matches 21; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Oy 11 EKAKKAYKAAEAKKAAKYEKAAEAKAAKAAKAA 42
 :||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 1 KKAAPAKKAAAPAKKAAAPAKKAAAKKAPAKKAA 32

RESULT 4
 ID ADF45561 standard; peptide; 39 AA.
 XX
 AC ADF45561;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Methylated HBHA peptide for vaccine against mycobacterial infections.
 XX
 KW vaccine; immunogen; methylation; heparin-binding hemagglutinin antigen;
 KW Mycobacterium bovis; Mycobacterium tuberculosis.
 XX
 OS Mycobacterium sp.
 XX
 PN FR2832410-Al.
 XX
 PD 23-MAY-2003.
 XX
 PF 19-NOV-2001; 2001FR-00014953.
 XX
 PR 19-NOV-2001; 2001FR-00014953.
 XX
 PA (INSP) INST PASTEUR LILLE.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX
 PI Pethe K, Menozzi F, Loch C;
 XX
 DR WPI; 2003-471775/45.
 XX
 PT New recombinant methylated mycobacterial heparin-binding hemagglutinin,
 PT useful as immunogen in anti-tuberculosis vaccines, also vectors for its
 PT preparation.
 XX
 PS Disclosure; Fig 2; 41pp; French.
 XX
 CC The invention relates to an immunogenic recombinant peptide which is the
 CC methylated form of an expression product of a nucleic acid that encodes a
 CC mycobacterial heparin-binding hemagglutinin antigen (HBHA), especially
 CC from Mycobacterium bovis BCG or M. tuberculosis. The peptide, also
 CC methylated native HBHA, is used to prepare vaccines against mycobacterial
 CC infections, particularly Mycobacterium bovis and M. tuberculosis. This
 CC peptide is the carboxyterminal of HBHA which binds to heparin.
 CC Methylation of this peptide occurs on the side chains of the lysine amino
 CC acids with either a methyl or dimethyl group.
 XX
 SQ Sequence 39 AA;

Query Match 40.4%; Score 86; DB 7; Length 39;
 Best Local Similarity 65.6%; Pred. No. 0.019;
 Matches 21; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Oy 11 EKAKKAYKAAEAKKAAKYEKAAEAKAAKAAKAA 42
 :||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 1 KKAAPAKKAAAPAKKAAAPAKKAAAKKAPAKKAA 32

RESULT 5
 ID AAR90180 standard; peptide; 32 AA.
 XX
 AC AAR90180;
 XX
 DT 25-MAR-1996 (first entry)
 XX
 DE Polycationic polypeptide n-protamine analogue.
 XX
 KW n-protamine; anticoagulation reversal; low molecular weight heparin;
 KW polycationic; positively charged amino acid; lysine.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal is acetylated"
 FT Modified-site 32 /note= "C-terminal is in amide form"
 FT
 XX WO9513083-Al.
 XX
 XX 18-MAY-1995.
 PD
 XX 10-NOV-1994; 94WO-US012981.
 PF
 XX 12-NOV-1993; 93US-00152488.
 PR
 XX 08-SEP-1994; 94US-00303025.
 XX
 XX (UNMI) UNIV MICHIGAN.
 XX
 PI Wakefield TW, Stanley JC, Andrews PC;
 XX
 DR WPI; 1995-193899/25.
 XX
 PT New poly:cationic polypeptide n-protamine analogues - having reduced
 PT cationic charge and lower toxicity, used for reversing (low mol.wt.)
 PT heparin anticoagulation.
 XX
 PS Disclosure; Page 13; 34pp; English.
 XX
 CC Novel peptides are claimed which contain 20-40 amino acids and which have
 CC a total cationic charge of less than +21 (pref. +16 to +18; esp. +18) as
 CC determined by the number of positively charged amino acids in the
 CC sequence. Preferably the positive charges are grouped in clusters
 CC separated by neutral amino acids. Especially the peptides contain 28-32
 CC amino acids having blocks of 2-4 positively charged amino acids separated
 CC by blocks of 2-6 neutral acids. Alternatively the positive charge may be
 CC distributed evenly or randomly along the peptide sequence. In particular
 CC the peptides are analogues of n-protamine (total cationic charge = +21)
 CC in which selected arginine residues have been replaced with uncharged
 CC amino acids and other arginine residues have been replaced by other
 CC positively charged amino acid residues, preferably lysine. The peptides
 CC reverse the effect of low mol. wt. heparin (LMWH) anticoagulation and
 CC hence can be used medically to prevent bleeding after the conclusion of
 CC clinical procedures using heparin therapy. They are less toxic than n-
 CC protamine since the reduced positive charge gives an improved efficiency
 CC to toxicity ratio; and they may be more effective than n-protamine in
 CC their anti-LMWH action. The present sequence (total cationic charge =
 CC +18) is a specific example of the new polypeptides
 XX
 SQ Sequence 32 AA;

Query Match 35.0%; Score 74.5; DB 2; Length 32;
 Best Local Similarity 68.8%; Pred. No. 0.27;
 Matches 22; Conservative 3; Mismatches 4; Indels 3; Gaps 2;

Qy 5 AKKAKAKKAYKAAEAKKAAKYEKAAAEKA 36
 ||||| :||||| :||||| :||||| :|||||
 Db 2 AKKA-AKKA--AKKAKKAAKKA--AKKA 30

RESULT 6
 AAW06686
 ID AAW06686 standard; peptide: 32 AA.
 AC AAW06686;
 DT 05-AUG-1997 (first entry)
 XX Protamine-like peptide analogue [+18B].
 XX Coagulation; anticoagulant; heparin; platelet aggregation; cell adhesion;
 XX positively charged cluster; arginine; polycationic; decreases;
 KW n-protamine; salmine protamine; protamine sulphate; salmon sperm.
 XX Synthetic.
 OS
 XX
 XX Key Location/Qualifiers
 FH Modified-site 1 /note= "acetylated"
 FT Region 3..30
 FT /label= repeat region
 FT /note= "4 tandem repeats of (Lys)2(Ala)2(Lys)2Ala motif"
 FT Modified-site 32
 FT /note= "amidated"
 XX
 XX W09635444-A1.
 XX
 XX 14-NOV-1996.
 XX
 XX 08-MAY-1996; 96WO-US006567.
 XX
 XX 08-MAY-1995; 95US-00436703.
 XX
 XX (UNMI) UNIV MICHIGAN.
 XX
 XX Wakefield TW, Stanley JC, Andrews PC;
 XX
 XX WPI; 1997-011697/01.
 XX
 XX Peptide reversing the anticoagulant effects of heparin - is based on
 XX protamine but has fewer positive charges for reduced toxicity.
 XX
 XX Disclosure; Page 5; 42pp; English.

Novel peptides are claimed which contain 20-40 amino acids and which have a total cationic charge of less than +21 (pref. +16 to +18; esp. +18) as determined by the number of positively charged amino acids in the sequence. Preferably the positive charges are grouped in clusters separated by neutral amino acids. Especially the peptides contain 28-32 amino acids having blocks of 2-4 positively charged amino acids separated by blocks of 2-6 neutral acids. Alternatively the positive charge may be distributed evenly or randomly along the peptide sequence. In particular the peptides are analogues of n-protamine (total cationic charge = +21) in which selected arginine residues have been replaced with uncharged amino acids and other arginine residues have been replaced by other positively charged amino acid residues, preferably lysine. The peptides reverse the effect of low mol. wt. heparin (LMWH) anticoagulation and hence can be used medically to prevent bleeding after the conclusion of clinical procedures using heparin therapy. They are less toxic than n-protamine since the reduced positive charge gives an improved efficiency to toxicity ratio; and they may be more effective than n-protamine in their anti-LMWH action. The present sequence [total cationic charge = +16] is a specific example of the new polypeptides

XX SQ Sequence 32 AA;
 Query Match 35.0%; Score 74.5; DB 2; Length 32;
 Best Local Similarity 68.8%; Pred. No. 0.27;
 Matches 22; Conservative 3; Mismatches 4; Indels 3; Gaps 2;

Qy 5 AKKAKAKKAYKAAEAKKAAKYEKAAAEKA 36
 ||||| :||||| :||||| :||||| :|||||
 Db 2 AKKA-AKKA--AKKAKKAAKKA--AKKA 30

RESULT 7
 AAR90181
 ID AAR90181 standard; peptide: 33 AA.
 XX AAR90181;
 AC AAR90181;
 DT 25-MAR-1996 (first entry)
 XX Polycationic polypeptide n-protamine analogue.
 XX n-protamine; anticoagulation reversal; low molecular weight heparin;
 KW polycationic; positively charged amino acid; lysine.
 XX Synthetic.
 OS
 XX
 XX Key Location/Qualifiers
 FH Modified-site 1 /note= "N-terminal is acetylated"
 FT Modified-site 33
 FT /note= "C-terminal is in amide form"
 XX W09513083-A1.
 XX
 XX 18-MAY-1995.
 XX
 XX 10-NOV-1994; 94WO-US012981.
 XX
 XX 12-NOV-1993; 93US-00152488.
 XX 08-SEP-1994; 94US-00303025.
 XX
 XX (UNMI) UNIV MICHIGAN.
 XX
 XX Wakefield TW, Stanley JC, Andrews PC;
 XX
 XX WPI; 1995-193899/25.
 XX
 XX New poly:cationic polypeptide n-protamine analogues - having reduced
 XX cationic charge and lower toxicity, used for reversing (low mol.wt.)
 XX heparin anticoagulation.
 XX
 XX Disclosure; Page 13; 34pp; English.

Novel peptides are claimed which contain 20-40 amino acids and which have a total cationic charge of less than +21 (pref. +16 to +18; esp. +18) as determined by the number of positively charged amino acids in the sequence. Preferably the positive charges are grouped in clusters separated by neutral amino acids. Especially the peptides contain 28-32 amino acids having blocks of 2-4 positively charged amino acids separated by blocks of 2-6 neutral acids. Alternatively the positive charge may be distributed evenly or randomly along the peptide sequence. In particular the peptides are analogues of n-protamine (total cationic charge = +21) in which selected arginine residues have been replaced with uncharged amino acids and other arginine residues have been replaced by other positively charged amino acid residues, preferably lysine. The peptides reverse the effect of low mol. wt. heparin (LMWH) anticoagulation and hence can be used medically to prevent bleeding after the conclusion of clinical procedures using heparin therapy. They are less toxic than n-protamine since the reduced positive charge gives an improved efficiency to toxicity ratio; and they may be more effective than n-protamine in their anti-LMWH action. The present sequence [total cationic charge = +16] is a specific example of the new polypeptides

XX SQ Sequence 33 AA;
Query Match 35.0%; Score 74.5; DB 2; Length 33;
Best Local Similarity 68.8%; Pred. No. 0.28;
Matches 22; Conservative 3; Mismatches 4; Indels 3; Gaps 2;
QY 5 AKKAERAKKAYKAAEAKKAAYEKAAAEKA 36
| | | | | : | | | | | : | | | | | : | | | | |
Db .3 AKKA- AKKA-- AKKAERAKKAYKAAEAKKAAYEKAAAEKA 31
RESULT 8
AAW06688
ID AAW06688 standard; peptide; 33 AA.
XX AC AAW06688;
XX DT 05-AUG-1997 (first entry)
XX XX Protamine-like peptide analogue [+18BE].
XX DE Coagulation; anticoagulant; heparin; platelet aggregation; cell adhesion;
KW positively charged cluster; arginine; polycationic; decrease;
KW n-protamine; salmine protamine; protamine sulphate; salmon sperm.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "acetylated"
FT Region 4..31
FT /label= repeat region
FT /note= "4 tandem repeats of (Lys)2(Ala)2 (Lys)2Ala motif"
FT Modified-site 33
FT /note= "amidated"
XX WO9635444-Al.
XX 14-NOV-1996.
XX 08-MAY-1996; 96WO-US006567.
XX 08-MAY-1995; 95US-00436703.
XX (UNMI) UNIV MICHIGAN.
XX Wakefield TW, Stanley JC, Andrews PC;
XX WPI; 1997-011697/01.
XX PT Peptide reversing the anticoagulant effects of heparin - is based on
XX PT protamine but has fewer positive charges for reduced toxicity.
XX PS Disclosure; Page 5; 42pp; English.
XX CC Protamine sulphate (also called n-protamine or salmine protamine) is a
XX CC polycationic peptide derived from salmon sperm and is used to reverse
XX CC heparin anticoagulation. One of the major components of salmine protamine
XX CC is a 32 amino acid peptide having a total cationic charge of [+21], with
XX CC arginine accounting for 67% of the total sequence and for all of the
XX CC positive charge. Peptides of 20-40 amino acids with total cationic charge
XX CC less than [+21] and which are able, at least partially, to reverse the
XX CC effect of heparin and/or low molecular weight heparin anticoagulants are
XX CC claimed. Specifically, the peptides are polycationic analogues of n-
XX CC protamine where the positive charge on the amino acid sequence is reduced
XX CC by selective replacement of positively charged arginine residues with an
XX CC unchanged residue, so that total cationic charge is less than [+21]. The
XX CC new peptides are used in vivo to reverse the effects of heparin; they
XX CC have the same anti-heparin activity as protamine but are less toxic
XX CC (because of the reduced number of positive charges) and are relatively
XX CC easy and inexpensive to prepare. The present sequence represents a
XX CC specific example of a protamine-like peptide with a charge of [+18] which

CC has been found to reverse the anticoagulation effects of both standard
XX and low molecular weight heparin
SQ Sequence 33 AA;
Query Match 35.0%; Score 74.5; DB 2; Length 33;
Best Local Similarity 68.8%; Pred. No. 0.28;
Matches 22; Conservative 3; Mismatches 4; Indels 3; Gaps 2;
QY 5 AKKAERAKKAYKAAEAKKAAYEKAAAEKA 36
| | | | | : | | | | | : | | | | | : | | | | |
Db 3 AKKA- AKKA-- AKKAERAKKAYKAAEAKKAAYEKAAAEKA 31
RESULT 9
AAB08170
ID AAB08170 standard; peptide; 40 AA.
XX AC AAB08170;
XX DT 04-DEC-2000 (first entry)
XX XX Peptide modulating activity of heparin, and other glycans.
XX DE Coagulation; anticoagulant; heparin; platelet aggregation; cell adhesion;
KW positively charged cluster; arginine; polycationic; decrease;
KW n-protamine; salmine protamine; protamine sulphate; salmon sperm.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "acetylated"
FT Region 4..31
FT /label= repeat region
FT /note= "4 tandem repeats of (Lys)2(Ala)2 (Lys)2Ala motif"
FT Modified-site 33
FT /note= "amidated"
XX WO9635444-Al.
XX 10-AUG-2000.
XX 02-FEB-2000; 2000WO-US002853.
XX 02-FEB-1999; 99US-0118276P.
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX San Antonio JD, Verrecchio A, Schick BP;
XX WPI; 2000-543446/49.
XX Novel synthetic peptides with high affinity for glycoaminoglycans and
XX PT proteoglycans, useful for modulating heparin, promoting cell attachment,
XX PT modulating tumor metastasis and modulating wound healing.
XX PS Disclosure; Page 30; 76pp; English.
XX CC The present sequence represents a synthetic peptide which has a high
XX CC affinity for glycoaminoglycans and proteoglycans. The peptide is useful
XX CC in methods for modulating heparin or other glycoaminoglycans with
XX CC anticoagulant activity, promoting cell attachment or adhesion to natural
XX CC or synthetic surfaces (especially vein grafts), modulating tumour cell
XX CC metastasis, modulating cartilage differentiation, targeting drugs to
XX CC epithelial cell surfaces (or to other cells expressing proteoglycans),
XX CC modulating enzymes that act on glycoaminoglycan substrates, affinity
XX CC purification of bioactive sequences of a glycoaminoglycan, modifying
XX CC endothelial cell pro-coagulant or anti-coagulant functions mediated
XX CC through glycoaminoglycans, and modulating wound healing. The peptide may
XX CC also be used for blocking tissue uptake of heparin or other
XX CC glycoaminoglycans in a mammal to increase heparin half-life in
XX CC circulation
SQ Sequence 40 AA;
Query Match 34.7%; Score 74; DB 3; Length 40;
Best Local Similarity 50.0%; Pred. No. 0.39;
Matches 21; Conservative 5; Mismatches 12; Indels 4; Gaps 1;
QY 1 AKKAYAKAEKAYKAAEAKKAAYEKAAAEKA 42
| | | | | : | | | | | : | | | | | : | | | | |

Db 1 ARKKAARAKAARAKAAR-----KKAARAKAARAKAARAKAAR 38

RESULT 10
AAR90178
ID AAR90178 standard; peptide; 29 AA.
XX AC AAR90178;
XX DT 25-MAR-1996 (first entry)
XX DE Polycationic polypeptide n-protamine analogue.
XX KW n-protamine; anticoagulation reversal; low molecular weight heparin;
XX KW polycationic; positively charged amino acid; lysine.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "N-terminal is acetylated"
FT Modified-site 29
FT /note= "C-terminal is in amide form"
XX WO9513083-A1.
XX 18-MAY-1995.
XX 10-NOV-1994; 94WO-US012981.
XX 12-NOV-1993; 93US-00152488.
XX 08-SEP-1994; 94US-00303025.
XX (UNMI) UNIV MICHIGAN.
XX Wakefield TW, Stanley JC, Andrews PC;
XX WPI; 1995-193899/25.
XX New poly:cationic polypeptide n-protamine analogues - having reduced
XX cationic charge and lower toxicity, used for reversing (low mol.wt.)
XX heparin anticoagulation.
XX Disclosure; Page 13; 34pp; English.
XX Novel peptides are claimed which contain 20-40 amino acids and which have
XX a total cationic charge of less than +21 (pref. +16 to +18; esp. +18) as
XX determined by the number of positively charged amino acids in the
XX sequence. Preferably the positive charges are grouped in clusters
XX separated by neutral amino acids. Especially the peptides contain 28-32
XX amino acids having blocks of 2-4 positively charged amino acids separated
XX by blocks of 2-6 neutral acids. Alternatively the positive charge may be
XX distributed evenly or randomly along the peptide sequence. In particular
XX the peptides are analogues of n-protamine (total cationic charge = +21)
XX in which selected arginine residues have been replaced with uncharged
XX amino acids and other arginine residues have been replaced by other
XX positively charged amino acid residues, preferably lysine. The peptides
XX reverse the effect of low mol. wt. heparin (LMWH) anticoagulation and
XX hence can be used medically to prevent bleeding after the conclusion of
XX clinical procedures using heparin therapy. They are less toxic than n-
XX protamine since the reduced positive charge gives an improved efficiency
XX to toxicity ratio; and they may be more effective than n-protamine in
XX their anti-LMWH action. The present sequence (total cationic charge =
XX +16) is a specific example of the new polypeptides
XX Sequence 29 AA;

Query Match 33.8%; Score 72; DB 2; Length 29;
Best Local Similarity 72.4%; Pred. No. 0.46;
Matches 21; Conservative 2; Mismatches 2; Indels 4; Gaps 2;

Qy 1 AKKYAKAK--AEKAKYAKAEAKKAAK 27
||| ||||| |:||||| |:|||||

Db 2 AKKAARAKAARAKAARAKAARAKAARAKAARAKAARAKAARAKAAR 28

RESULT 11
AAR90176
ID AAR90176 standard; peptide; 29 AA.
XX AC AAR90176;
XX DT 25-MAR-1996 (first entry)
XX DE Polycationic polypeptide n-protamine analogue.
XX KW n-protamine; anticoagulation reversal; low molecular weight heparin;
XX KW polycationic; positively charged amino acid; lysine.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "N-terminal can be acetylated"
FT Modified-site 29
FT /note= "C-terminal can be in amide form"
XX WO9513083-A1.
XX 18-MAY-1995.
XX 10-NOV-1994; 94WO-US012981.
XX 12-NOV-1993; 93US-00152488.
XX 08-SEP-1994; 94US-00303025.
XX (UNMI) UNIV MICHIGAN.
XX Wakefield TW, Stanley JC, Andrews PC;
XX WPI; 1995-193899/25.
XX New poly:cationic polypeptide n-protamine analogues - having reduced
XX cationic charge and lower toxicity, used for reversing (low mol.wt.)
XX heparin anticoagulation.
XX Disclosure; Page 13; 34pp; English.
XX Novel peptides are claimed which contain 20-40 amino acids and which have
XX a total cationic charge of less than +21 (pref. +16 to +18; esp. +18) as
XX determined by the number of positively charged amino acids in the
XX sequence. Preferably the positive charges are grouped in clusters
XX separated by neutral amino acids. Especially the peptides contain 28-32
XX amino acids having blocks of 2-4 positively charged amino acids separated
XX by blocks of 2-6 neutral acids. Alternatively the positive charge may be
XX distributed evenly or randomly along the peptide sequence. In particular
XX the peptides are analogues of n-protamine (total cationic charge = +21)
XX in which selected arginine residues have been replaced with uncharged
XX amino acids and other arginine residues have been replaced by other
XX positively charged amino acid residues, preferably lysine. The peptides
XX reverse the effect of low mol. wt. heparin (LMWH) anticoagulation and
XX hence can be used medically to prevent bleeding after the conclusion of
XX clinical procedures using heparin therapy. They are less toxic than n-
XX protamine since the reduced positive charge gives an improved efficiency
XX to toxicity ratio; and they may be more effective than n-protamine in
XX their anti-LMWH action. The present sequence (total cationic charge =
XX +16) is a specific example of the new polypeptides
XX Sequence 29 AA;

Query Match 33.8%; Score 72; DB 2; Length 29;
Best Local Similarity 72.4%; Pred. No. 0.46;
Matches 21; Conservative 2; Mismatches 2; Indels 4; Gaps 2;

Qy 1 AKKYAKAK--AEKAKYAKAEAKKAAK 27
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Matches 21; Conservative 2; Mismatches 2; Indels 4; Gaps 2;

Qy 1 AKYAKAK--AEKAKYKAAAEKAKAK 27
 ||| ||||| |:||||| |:|||||
 Db 2 AKKAAKAKKAAKAKKAA--AKKAKKAAK 28
 ||| ||||| |:||||| |:|||||

RESULT 14
 AAB08175
 ID AAB08175 standard; peptide; 32 AA.
 XX AAB08175;
 XX
 XX 04-DEC-2000 (first entry)
 XX
 XX Peptide modulating activity of heparin, and other glycans.
 XX
 XX Glycoaminoglycan; proteoglycan; heparin modulation; anticoagulant;
 KW cell attachment; cell adhesion; vein graft; tumour cell metastasis;
 KW cartilage differentiation; wound healing.
 XX
 XX Synthetic.
 OS
 XX WO200045831-A1.
 FN
 XX 10-AUG-2000.
 PD
 XX 02-FEB-2000; 2000WO-US002853.
 PF
 XX 02-FEB-1999; 99US-0118276P.
 PR
 XX (UYJE-) UNIV JEFFERSON THOMAS.
 PA
 XX San Antonio JD, Verrecchio A, Schick BP;
 PI
 XX WPI; 2000-543446/49.
 DR
 XX Novel synthetic peptides with high affinity for glycoaminoglycans and
 XX proteoglycans, useful for modulating heparin, promoting cell attachment,
 PT modulating tumor metastasis and modulating wound healing.
 PT
 XX Disclosure; Page 31; 76pp; English.
 PS
 XX The present sequence represents a synthetic peptide which has a high
 CC affinity for glycoaminoglycans and proteoglycans. The peptide is useful
 CC in methods for modulating heparin or other glycoaminoglycans with
 CC anticoagulant activity, promoting cell attachment or adhesion to natural
 CC or synthetic surfaces (especially vein grafts), modulating tumour cell
 CC metastasis, modulating cartilage differentiation, targeting drugs to
 CC epithelial cell surfaces (or to other cells expressing proteoglycans),
 CC modulating enzymes that act on glycoaminoglycan substrates, affinity
 CC purification of bioactive sequences of a glycoaminoglycan, modifying
 CC endothelial cell pro-coagulant or anti-coagulant functions mediated
 CC through glycoaminoglycans, and modulating wound healing. The peptide may
 CC also be used for blocking tissue uptake of heparin or other
 CC glycoaminoglycans in a mammal to increase heparin half-life in
 CC circulation
 XX
 SQ Sequence 32 AA;
 Query Match 32.4%; Score 69; DB 3; Length 32;
 Best Local Similarity 62.1%; Pred. No. 1.1;
 Matches 18; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 11 EKAKYKAAAEKAKYKAAAEKAKAK 39
 :||| ||| ||||| ||||| |||||
 Db 3 KKAACAAAAAARKKAAKAAKAAKAAK 31
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RESULT 15
 AAB08169
 ID AAB08169 standard; peptide; 36 AA.
 XX

AC AAB08169;
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE Peptide modulating activity of heparin, and other glycans.
 XX
 KW Glycoaminoglycan; proteoglycan; heparin modulation; anticoagulant;
 KW cell attachment; cell adhesion; vein graft; tumour cell metastasis;
 KW cartilage differentiation; wound healing.
 XX
 OS Synthetic.
 XX WO200045831-A1.
 FN
 XX 10-AUG-2000.
 PD
 XX 02-FEB-2000; 2000WO-US002853.
 PF
 XX 02-FEB-1999; 99US-0118276P.
 PR
 XX (UYJE-) UNIV JEFFERSON THOMAS.
 PA
 XX San Antonio JD, Verrecchio A, Schick BP;
 PI
 XX WPI; 2000-543446/49.
 DR
 XX Novel synthetic peptides with high affinity for glycoaminoglycans and
 XX proteoglycans, useful for modulating heparin, promoting cell attachment,
 PT modulating tumor metastasis and modulating wound healing.
 PT
 XX Disclosure; Page 30; 76pp; English.
 PS
 XX The present sequence represents a synthetic peptide which has a high
 CC affinity for glycoaminoglycans and proteoglycans. The peptide is useful
 CC in methods for modulating heparin or other glycoaminoglycans with
 CC anticoagulant activity, promoting cell attachment or adhesion to natural
 CC or synthetic surfaces (especially vein grafts), modulating tumour cell
 CC metastasis, modulating cartilage differentiation, targeting drugs to
 CC epithelial cell surfaces (or to other cells expressing proteoglycans),
 CC modulating enzymes that act on glycoaminoglycan substrates, affinity
 CC purification of bioactive sequences of a glycoaminoglycan, modifying
 CC endothelial cell pro-coagulant or anti-coagulant functions mediated
 CC through glycoaminoglycans, and modulating wound healing. The peptide may
 CC also be used for blocking tissue uptake of heparin or other
 CC glycoaminoglycans in a mammal to increase heparin half-life in
 CC circulation
 XX
 SQ Sequence 36 AA;
 Query Match 31.9%; Score 68; DB 3; Length 36;
 Best Local Similarity 58.3%; Pred. No. 1.6;
 Matches 21; Conservative 5; Mismatches 8; Indels 2; Gaps 2;

Qy 5 AKKAK-REKAKYKAAAEKAKYKAAAEKAKAA 38
 ||||| :||| :||| ||||| :||| :||| :|||
 Db 1 AKKAAKAAKAAKAAKAAKAAKAAKAAKAAK 36
 ||||| :||| :||| ||||| :||| :||| :|||

Search completed: June 3, 2005, 10:15:30
 Job time : 158 secs

RESULT 2


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; Publication No. US20030100496A1
; GENERAL INFORMATION:
; APPLICANT: Haines, Adrian M
; APPLICANT: Phillips, Ross O
; APPLICANT: Welsh, John H
; APPLICANT: Thatcher, David R
; APPLICANT: Irvine, Alistair S
; TITLE OF INVENTION: Compositions and Methods for Highly Efficient Transfection
; FILE REFERENCE: CACO0063
; CURRENT APPLICATION NUMBER: US/10/219,626
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 09/023,406
; PRIOR FILING DATE: 1998-02-12
; PRIOR APPLICATION NUMBER: 09/022,614
; PRIOR FILING DATE: 1998-02-12
; PRIOR APPLICATION NUMBER: 08/861,283
; PRIOR FILING DATE: 1997-05-21
; PRIOR APPLICATION NUMBER: 08/800,079
; PRIOR FILING DATE: 1997-02-12
; PRIOR APPLICATION NUMBER: 9602777.6
; PRIOR FILING DATE: 1996-02-12
; PRIOR APPLICATION NUMBER: 9614548.7
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 08/861,432
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic construct
US-10-219-626-5

Query Match      29.3%; Score 62.5; DB 14; Length 38;
Best Local Similarity 51.4%; Pred. No. 4.9;
Matches 19; Conservative 3; Mismatches 14; Indels 1; Gaps 1;

Qy 2 KKYAKKAERKAKKAYKAAEAARAKKAAKAAKAAKAA 38
Db 2 KKSPPKAKPKPAKSPKPAK-KPAKSPKPAKPAK 37

RESULT 7
US-10-437-963-192079
; Sequence 192079, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 192079
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_88338C.1.pep
US-10-437-963-192079

Query Match      29.1%; Score 62; DB 16; Length 43;
Best Local Similarity 44.1%; Pred. No. 6.3;

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Matches 15; Conservative 2; Mismatches 17; Indels 0; Gaps 0;

Qy 2 KKYAKKAERKAKKAYKAAEAARAKKAAKAAKAAKAA 35
Db 2 KKYAKKAERKAKKAYKAAEAARAKKAAKAAKAAKAA 35

RESULT 8
US-10-424-599-200302
; Sequence 200302, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 200302
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_2289C.1.pep
US-10-424-599-200302

Query Match      28.6%; Score 61; DB 15; Length 42;
Best Local Similarity 41.0%; Pred. No. 7.9;
Matches 16; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

Qy 2 KKYAKKAERKAKKAYKAAEAARAKKAAKAAKAAKAA 40
Db 2 KKYAKKAERKAKKAYKAAEAARAKKAAKAAKAAKAA 40

RESULT 9
US-10-667-004-21
; Sequence 21, Application US/10667004
; Publication No. US20040126820A1
; GENERAL INFORMATION:
; APPLICANT: INTEL CORPORATION
; APPLICANT: CHAN, Selena
; APPLICANT: SU, Xing
; APPLICANT: YAMAKAWA, Mineo
; TITLE OF INVENTION: CONTROLLED ALIGNMENT OF NANO-BARCODES ENCODING SPECIFIC INFORMATION
; FILE REFERENCE: INTEL1310-1(P14240X)
; CURRENT APPLICATION NUMBER: US/10/667,004
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US 10/251,152
; PRIOR FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 21
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-667-004-21

Query Match      28.2%; Score 60; DB 16; Length 28;
Best Local Similarity 60.0%; Pred. No. 6.5;
Matches 18; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

Qy 5 AKKAAERKAKKAYKAAEAARAKKAAKAAKAAKAA 34
Db 1 AKKAAERKAKKAYKAAEAARAKKAAKAAKAAKAA 28

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RESULT 10
US-10-667-004-26
; Sequence 26, Application US/10667004
; Publication No. US20040126820A1
; GENERAL INFORMATION:
; APPLICANT: INTEL CORPORATION
; APPLICANT: CHAN, Selena
; APPLICANT: SU, Xing
; APPLICANT: YAMAKAWA, Mineo
; TITLE OF INVENTION: CONTROLLED ALIGNMENT OF NANO-BARCODES ENCODING SPECIFIC INFORMATION
; TITLE OF INVENTION: SCANNING PROBE MICROSCOPY (SPM)
; FILE REFERENCE: INTEL1310-1(P14240X)
; CURRENT APPLICATION NUMBER: US/10/667,004
; PRIOR FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US 10/251,152
; PRIOR FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-667-004-26

Query Match      28.2%; Score 60; DB 16; Length 28;
Best Local Similarity 60.0%; Pred. No. 6.5;
Matches 18; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

Qy      5 AKKAAKAKAKKAYKAAEAKKAAKAAEAKAAE 34
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Db      1 AAKAAAEAKAAAEAKAA--AAEAKAAAE 28

RESULT 11
US-09-805-301-32
; Sequence 32, Application US/09805301
; Patent No. US20020173456A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Louis C.
; Sparrow, James T.
; Hauer, Jochen
; Mims, Martha P.
; TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
; COMPUTER READABLE FORM:
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 6.0
; SOFTWARE: Word Perfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/805,301
; FILING DATE: 12-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/584,043
; FILING DATE: <Unknown>
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 217/189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-805-301-33
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-805-301-32

Query Match      27.7%; Score 59; DB 9; Length 38;
Best Local Similarity 39.5%; Pred. No. 12;
Matches 15; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

Qy      2 KKYAKKAKAKKAYKAAEAKKAAKAAEAKAAK 39
      |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      1 KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK 38

RESULT 12
US-09-805-301-33
; Sequence 33, Application US/09805301
; Patent No. US20020173456A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Louis C.
; Sparrow, James T.
; Hauer, Jochen
; Mims, Martha P.
; TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
; COMPUTER READABLE FORM:
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 6.0
; SOFTWARE: Word Perfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/805,301
; FILING DATE: 12-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/584,043
; FILING DATE: <Unknown>
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 217/189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-805-301-33
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Query Match 27.7%; Score 59; DB 9; Length 39;
 Best Local Similarity 39.5%; Pred. No. 12;
 Matches 15; Conservative 4; Mismatches 19; Indels 0; Gaps 0;
 QY 2 KKYAKKAAEKAKYKAAAEAKKAAKAAEKAAAEKAAK 39
 Db 2 KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK 39

RESULT 13
 US-09-805-301-34
 ; Sequence 34, Application US/09805301
 ; Patent No. US20020173456A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Smith, Louis C.
 ; Sparrow, James T.
 ; Hauer, Jochen
 ; Mims, Martha P.
 ; TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
 ; MACROMOLECULE DELIVERY
 ; NUMBER OF SEQUENCES: 139
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 6.0
 ; SOFTWARE: Word Perfect 6.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/805,301
 ; FILING DATE: 12-Mar-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/584,043
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard J.
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 217/189
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 34:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 40 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 34:
 US-09-805-301-34

Query Match 27.7%; Score 59; DB 9; Length 40;
 Best Local Similarity 39.5%; Pred. No. 12;
 Matches 15; Conservative 4; Mismatches 19; Indels 0; Gaps 0;
 QY 2 KKYAKKAAEKAKYKAAAEAKKAAKAAEKAAAEKAAK 39
 Db 3 KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK 40

RESULT 14
 US-09-805-301-35
 ; Sequence 35, Application US/09805301

; Patent No. US20020173456A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Smith, Louis C.
 ; Sparrow, James T.
 ; Hauer, Jochen
 ; Mims, Martha P.
 ; TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
 ; MACROMOLECULE DELIVERY
 ; NUMBER OF SEQUENCES: 139
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 6.0
 ; SOFTWARE: Word Perfect 6.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/805,301
 ; FILING DATE: 12-Mar-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/584,043
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard J.
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 217/189
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 35:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 41 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 35:
 US-09-805-301-35

Query Match 27.7%; Score 59; DB 9; Length 41;
 Best Local Similarity 39.5%; Pred. No. 13;
 Matches 15; Conservative 4; Mismatches 19; Indels 0; Gaps 0;
 QY 2 KKYAKKAAEKAKYKAAAEAKKAAKAAEKAAAEKAAK 39
 Db 4 KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK 41

RESULT 15
 US-09-805-301-36
 ; Sequence 36, Application US/09805301
 ; Patent No. US20020173456A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Smith, Louis C.
 ; Sparrow, James T.
 ; Hauer, Jochen
 ; Mims, Martha P.
 ; TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
 ; MACROMOLECULE DELIVERY
 ; NUMBER OF SEQUENCES: 139
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; Suite 4700


```

; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 6.0
; SOFTWARE: Word Perfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/805.301
; FILING DATE: 12-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/584,043
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 217/189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-805-301-36

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Query Match      27.7%; Score 59; DB 9; Length 42;
Best Local Similarity 39.5%; Pred.No. 13;
Matches 15; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

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Oy 2 KKYAKKAKAEKAKYKAAAEKAKYKAAAEKAAK 39
Db 5 KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKVTR 42

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Search completed: June 3, 2005, 10:31:26
Job time : 138 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	213	100.0	45	4	US-09-405-743A-2	Sequence 2, Appli
2	213	100.0	45	4	US-09-816-989A-2	Sequence 2, Appli
3	108	50.7	35	4	US-09-405-743A-1	Sequence 1, Appli
4	108	50.7	35	4	US-09-816-989A-1	Sequence 1, Appli
5	74.5	35.0	32	1	US-08-152-488-13	Sequence 13, Appl
6	74.5	35.0	32	1	US-08-303-025-15	Sequence 15, Appl
7	74.5	35.0	32	1	US-08-677-304-13	Sequence 13, Appl
8	74.5	35.0	32	2	US-08-436-703B-2	Sequence 2, Appli
9	74.5	35.0	33	1	US-08-303-025-16	Sequence 16, Appl
10	74.5	35.0	33	2	US-08-436-703B-4	Sequence 4, Appli
11	72	33.8	29	1	US-08-152-488-10	Sequence 10, Appl
12	72	33.8	29	1	US-08-152-488-11	Sequence 11, Appl
13	72	33.8	29	1	US-08-303-025-10	Sequence 10, Appl
14	72	33.8	29	1	US-08-303-025-11	Sequence 11, Appl
15	72	33.8	29	1	US-08-303-025-13	Sequence 13, Appl
16	72	33.8	29	1	US-08-677-304-10	Sequence 10, Appl
17	72	33.8	29	1	US-08-677-304-11	Sequence 11, Appl
18	72	33.8	29	2	US-08-436-703B-3	Sequence 3, Appli
19	72	33.8	29	2	US-08-436-703B-15	Sequence 15, Appl
20	67	31.5	28	1	US-08-303-025-12	Sequence 12, Appl
21	67	31.5	28	2	US-08-436-703B-1	Sequence 1, Appli
22	67	31.5	28	3	US-09-117-121-24	Sequence 24, Appl
23	66	31.0	29	1	US-08-152-488-12	Sequence 12, Appl
24	66	31.0	29	1	US-08-303-025-14	Sequence 14, Appl
25	66	31.0	29	2	US-08-677-304-12	Sequence 12, Appl
26	66	31.0	29	2	US-08-436-703B-16	Sequence 16, Appl
27	64	30.0	38	3	US-09-117-121-16	Sequence 16, Appl

Query Match 50.7%; Score 108; DB 4; Length 35;
Best Local Similarity 64.4%; Pred. No. 2.4e-05;

RESULT 6
US-08-303-025-15

; Sequence 15, Application US/08303025
; Patent No. 5614494
; GENERAL INFORMATION:
; APPLICANT: Wakefield, Thomas W.
; APPLICANT: Andrews, Philip C.
; APPLICANT: Stanley, James C.
; TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
; TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
; TITLE OF INVENTION: ANTICOAGULATION REVERSAL
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Benita J. Rohm, Esq.
; STREET: 150 West Jefferson, Suite 2500
; CITY: Detroit
; STATE: Michigan
; COUNTRY: United States of America
; ZIP: 48226-4415
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy diskette 3.5" 1.44Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS V.6.22
; SOFTWARE: WordPerfect 6.1; ASCII (DOS)Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/303,025
; FILING DATE: 08-SEPT-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06829
; FILING DATE: 14-AUG-1992
; APPLICATION NUMBER: US 08/152,488
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rohm, Benita J.
; REFERENCE/DOCKET NUMBER: 7WH-060548-00231
; TELEPHONE: 313-496-7622
; TELEFAX: 313-496-8454
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: N/A
; TOPOLOGY: N/A
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: N/A
; PUBLICATION INFORMATION:
; AUTHORS: N/A
; TITLE: N/A
; DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
; US-08-303-025-15

Query Match 35.0%; Score 74.5; DB 1; Length 32;
Best Local Similarity 68.8%; Pred. No. 0.081; 4; Indels 3; Gaps 2;
Matches 22; Conservative 3; Mismatches 4; Indels 3; Gaps 2;

Qy 5 AKKAAEKAKYKAAEAKKAAKYEKAAAEKA 36
Db 2 AKKA-AKKAKKA--AKKAKKAAKKAKEKA 30

RESULT 7
US-08-677-304-13
; Sequence 13, Application US/08677304
; Patent No. 5721212
; GENERAL INFORMATION:
; APPLICANT: Wakefield, Thomas W.
; APPLICANT: Andrews, Philip C.
; APPLICANT: Stanley, James C.
; TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
; TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
; TITLE OF INVENTION: ANTICOAGULATION REVERSAL

; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Benita J. Rohm, Esq.
; STREET: 512 Springfield Avenue
; CITY: Cranford
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07016-1811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6; ASCII (DOS)Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,304
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/152,488
; FILING DATE: 12-NOV-1993
; APPLICATION NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rohm, Benita J.
; REGISTRATION NUMBER: 28,664
; REFERENCE/DOCKET NUMBER: RM-7WG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-276-3344
; TELEFAX: 908-276-5543
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: No. 5721212 Relevant
; TOPOLOGY: No. 5721212 Relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: N/A
; PUBLICATION INFORMATION:
; AUTHORS: N/A
; TITLE: N/A
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
; US-08-677-304-13

Query Match 35.0%; Score 74.5; DB 1; Length 32;
Best Local Similarity 68.8%; Pred. No. 0.081; 4; Indels 3; Gaps 2;
Matches 22; Conservative 3; Mismatches 4; Indels 3; Gaps 2;

Qy 5 AKKAAEKAKYKAAEAKKAAKYEKAAAEKA 36
Db 2 AKKA-AKKAKKA--AKKAKKAAKKAKEKA 30

RESULT 8
US-08-436-703B-2
; Sequence 2, Application US/08436703B
; Patent No. 5919761
; GENERAL INFORMATION:
; APPLICANT: Wakefield, Thomas W.
; APPLICANT: Andrews, Philip C.
; APPLICANT: Stanley, James C.
; TITLE OF INVENTION: NOVEL PEPTIDES FOR
; TITLE OF INVENTION: HEPARIN AND LOW MOLECULAR
; TITLE OF INVENTION: WEIGHT HEPARIN
; TITLE OF INVENTION: ANTICOAGULATION REVERSAL
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Benita J. Rohm, Esq.
; STREET: 6601 Woodward Avenue
; STREET: Suite 1525
; CITY: Detroit

STATE: Michigan
COUNTRY: United States of America
ZIP: 48226
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk 1.44Mb, 3.5"
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6;
SOFTWARE: ASCII (DOS)Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436.703B
FILING DATE: 08-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: N/A
FILING DATE: N/A
ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
REGISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: 7WK-060548-00233
TELECOMMUNICATION INFORMATION:
TELEPHONE: 313-965-1976
TELEFAX: 313-965-1951
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SOURCE: N/A
ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
TITLE: N/A
US-08-436-703B-2

Query Match 35.0%; Score 74.5; DB 2; Length 32;
Best Local Similarity 68.8%; Pred. No. 0.081; 4; Indels 3; Gaps 2;
Matches 22; Conservative 3; Mismatches 4; Indels 3; Gaps 2;

Qy 5 AKKAKAEKAKYKAAEAKKAAKYKAAEAKKA 36
Db 2 AKKA-AKKAKKA--AKKAKKAAKKAKKAAKKA 30

RESULT 9
US-08-303-025-16
Sequence 16, Application US/08303025
Patent No. 5614494
GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
TITLE OF INVENTION: ANTICOAGULATION REVERSAL
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J. Rohm, Esq.
STREET: 150 West Jefferson, Suite 2500
CITY: Detroit
STATE: Michigan
COUNTRY: United States of America
ZIP: 48226-4415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette 3.5" 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS v.6.22
SOFTWARE: WordPerfect 6.1; ASCII (DOS)Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303.025
FILING DATE: 08-SEPT-1994

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06829
FILING DATE: 14-AUG-1992
APPLICATION NUMBER: US 08/152,488
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
REFERENCE/DOCKET NUMBER: 7WH-060548-00231
TELECOMMUNICATION INFORMATION:
TELEPHONE: 313-496-7622
TELEFAX: 313-496-8454
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SOURCE: N/A
ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
TITLE: N/A
DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
US-08-303-025-16

Query Match 35.0%; Score 74.5; DB 1; Length 33;
Best Local Similarity 68.8%; Pred. No. 0.083;
Matches 22; Conservative 3; Mismatches 4; Indels 3; Gaps 2;

Qy 5 AKKAKAEKAKYKAAEAKKAAKYKAAEAKKA 36
Db 3 AKKA-AKKAKKA--AKKAKKAAKKAKKAAKKA 31

RESULT 10
US-08-436-703B-4
Sequence 4, Application US/08436703B
Patent No. 5919761
GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR
TITLE OF INVENTION: HEPARIN AND LOW MOLECULAR
TITLE OF INVENTION: WEIGHT HEPARIN
TITLE OF INVENTION: ANTICOAGULATION REVERSAL
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J. Rohm, Esq.
STREET: 6601 Woodward Avenue
CITY: Detroit
STATE: Michigan
COUNTRY: United States of America
ZIP: 48226
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk 1.44Mb, 3.5"
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6;
SOFTWARE: ASCII (DOS)Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436.703B
FILING DATE: 08-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: N/A
FILING DATE: N/A
ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.

REGISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: 7WK-060548-00233
TELECOMMUNICATION INFORMATION:
TELEPHONE: 313-965-1976
TELEFAX: 313-965-1951
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SOURCE: N/A
ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
TITLE: N/A
US-08-436-703B-4

Query Match 35.0%; Score 74.5; DB 2; Length 33;
Best Local Similarity 68.8%; Pred. No. 0.083;
Matches 22; Conservative 3; Mismatches 4; Indels 3; Gaps 2;

Qy	5	AKKAAEKA KAYKAAEA FAKAAAEK A	36
Db	3	AKKA-AKKAKKA-- AKKAKKA AKKAKKA AKKAKKA AKKAKKA	31

```

RESULT 11
US-08-152-488-10
; Sequence 10, Application US/08152488
; Patent No. 5534619
; GENERAL INFORMATION:
; APPLICANT: Wakefield, Thomas W.
; APPLICANT: Andrews, Philip C.
; APPLICANT: Stanley, James C.
; TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
; TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
; TITLE OF INVENTION: ANTICOAGULATION REVERSAL
; NUMBER OF SEQUENCES: 13

```

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Benita J. Rohm, Esq.
 STREET: 512 Springfield Avenue
 CITY: Cranford
 STATE: New Jersey
 COUNTRY: United States of America
 ZIP: 07016-1811
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WordPerfect 6; ASCII (DOS)Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/152,488
 FILING DATE: 12-NOV-1993
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/08069
 FILING DATE: 14-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Rohm, Benita J.
 REGISTRATION NUMBER: 28,664
 REFERENCE/DOCKET NUMBER: RM-7WG
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 908-276-3344
 TELEFAX: 908-276-5543
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29 amino acids
 TYPE: amino acid
 STRANDEDNESS: N/A
 TOPOLOGY: N/A
 MOLECULE TYPE: peptide

ORIGINAL SOURCE: N/A
ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
TITLE: N/A
PUBLICATION INFORMATION:
DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
US-08-152-488-10

Query Match 33.8%; Score 72; DB 1; Length 29;
Best Local Similarity 72.4%; Pred. No. 0.14;
Matches 21; Conservative 2; Mismatches 2; Indels 4; Gaps 2;

Qy	1	AKVAKAK--AEKAKAYKAAEAKKAAK	27
		: :	
Dp	2	AKAAAKAKKAAKAAKAA--AKAAKAAK	28

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RESULT 12
US-08-152-488-11
; Sequence 11, Application US/08152488
; Patent No. 5534619
; GENERAL INFORMATION:
; APPLICANT: Wakefield, Thomas W.
; APPLICANT: Andrews, Philip C.
; APPLICANT: Stanley, James C.
; TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
; TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
; TITLE OF INVENTION: ANTICOAGULATION REVERSAL
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:

```

ADDRESSEE: Benita J. Rohm, Esq.
STREET: 512 Springfield Avenue
CITY: Cranford
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07016-1811
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 6; ASCII (DOS) Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/152,488
FILING DATE: 12-NOV-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
REGISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: RM-7WG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-276-3344
TELEFAX: 908-276-5543
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
TITLE: N/A
PUBLICATION INFORMATION:
DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
US-08-152-488-11

Query Match 33.8%; Score 72; DB 1; Length 29;
 Best Local Similarity 72.4%; Pred. No. 0.14;
 Matches 21; Conservative 2; Mismatches 2; Indels 4; Gaps 2;

Qy 1 AKYAKKAK--AEKAKKAYKAAEAKKAAK 27
 ||| ||||| |:||||| |:|||||
 Db 2 AKGAKKAKKAAKKAKKA--AKKAKKAAK 28

RESULT 13

US-08-303-025-10
 ; Sequence 10, Application US/08303025
 ; Patent No. 5614494
 ; GENERAL INFORMATION:
 ; APPLICANT: Wakefield, Thomas W.
 ; APPLICANT: Andrews, Philip C.
 ; APPLICANT: Stanley, James C.
 ; TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
 ; TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
 ; TITLE OF INVENTION: ANTICOAGULATION REVERSAL
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Benita J. Rohm, Esq.
 ; STREET: 150 West Jefferson, Suite 2500
 ; CITY: Detroit
 ; STATE: Michigan
 ; COUNTRY: United States of America
 ; ZIP: 48226-4415
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy diskette 3.5" 1.44Mb
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: MS-DOS v.6.22
 ; SOFTWARE: WordPerfect 6.1; ASCII (DOS) Text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/303.025
 ; FILING DATE: 08-SEPT-1994
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US92/06829
 ; FILING DATE: 14-AUG-1992
 ; APPLICATION NUMBER: US 08/152,488
 ; FILING DATE: 12-NOV-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Rohm, Benita J.
 ; REFERENCE/DOCKET NUMBER: 7WH-060548-00231
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 313-496-7622
 ; TELEFAX: 313-496-8454
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 29 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: N/A
 ; TOPOLOGY: N/A
 ; MOLECULE TYPE: peptide
 ; ORIGINAL SOURCE:
 ; ORGANISM: N/A
 ; PUBLICATION INFORMATION:
 ; AUTHORS: N/A
 ; TITLE: N/A
 ; DOCUMENT NUMBER: PCT/US92/08069
 ; FILING DATE: 14-AUG-1993
 ; US-08-303-025-10

Query Match 33.8%; Score 72; DB 1; Length 29;
 Best Local Similarity 72.4%; Pred. No. 0.14;
 Matches 21; Conservative 2; Mismatches 2; Indels 4; Gaps 2;

Qy 1 AKYAKKAK--AEKAKKAYKAAEAKKAAK 27
 ||| ||||| |:||||| |:|||||
 Db 2 AKGAKKAKKAAKKAKKA--AKKAKKAAK 28

RESULT 14

US-08-303-025-11
 ; Sequence 11, Application US/08303025
 ; Patent No. 5614494
 ; GENERAL INFORMATION:
 ; APPLICANT: Wakefield, Thomas W.
 ; APPLICANT: Andrews, Philip C.
 ; APPLICANT: Stanley, James C.
 ; TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
 ; TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
 ; TITLE OF INVENTION: ANTICOAGULATION REVERSAL
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Benita J. Rohm, Esq.
 ; STREET: 150 West Jefferson, Suite 2500
 ; CITY: Detroit
 ; STATE: Michigan
 ; COUNTRY: United States of America
 ; ZIP: 48226-4415
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy diskette 3.5" 1.44Mb
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: MS-DOS v.6.22
 ; SOFTWARE: WordPerfect 6.1; ASCII (DOS) Text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/303.025
 ; FILING DATE: 08-SEPT-1994
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US92/06829
 ; FILING DATE: 14-AUG-1992
 ; APPLICATION NUMBER: US 08/152,488
 ; FILING DATE: 12-NOV-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Rohm, Benita J.
 ; REFERENCE/DOCKET NUMBER: 7WH-060548-00231
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 313-496-7622
 ; TELEFAX: 313-496-8454
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 29 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: N/A
 ; TOPOLOGY: N/A
 ; MOLECULE TYPE: peptide
 ; ORIGINAL SOURCE:
 ; ORGANISM: N/A
 ; PUBLICATION INFORMATION:
 ; AUTHORS: N/A
 ; TITLE: N/A
 ; DOCUMENT NUMBER: PCT/US92/08069
 ; FILING DATE: 14-AUG-1993
 ; US-08-303-025-11

Query Match 33.8%; Score 72; DB 1; Length 29;
 Best Local Similarity 72.4%; Pred. No. 0.14;
 Matches 21; Conservative 2; Mismatches 2; Indels 4; Gaps 2;

Qy 1 AKYAKKAK--AEKAKKAYKAAEAKKAAK 27
 ||| ||||| |:||||| |:|||||
 Db 2 AKGAKKAKKAAKKAKKA--AKKAKKAAK 28

RESULT 15

US-08-303-025-13
 ; Sequence 13, Application US/08303025
 ; Patent No. 5614494
 ; GENERAL INFORMATION:
 ; APPLICANT: Wakefield, Thomas W.
 ; APPLICANT: Andrews, Philip C.
 ; APPLICANT: Stanley, James C.

; TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
 ; TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
 ; TITLE OF INVENTION: ANTICOAGULATION REVERSAL
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Benita J. Rohm, Esq.
 ; STREET: 150 West Jefferson, Suite 2500
 ; CITY: Detroit
 ; STATE: Michigan
 ; COUNTRY: United States of America
 ; ZIP: 48226-4415
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy diskette 3.5" 1.44Mb
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: MS-DOS V.6.22
 ; SOFTWARE: WordPerfect 6.1; ASCII (DOS)Text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/303,025
 ; FILING DATE: 08-SEPT-1994
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US92/06829
 ; FILING DATE: 14-AUG-1992
 ; APPLICATION NUMBER: US 08/152,488
 ; FILING DATE: 12-NOV-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Rohm, Benita J.
 ; REFERENCE/DOCKET NUMBER: 7WH-060548-00231
 ; TELEPHONE: 313-496-7622
 ; TELEFAX: 313-496-8454
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 29 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: N/A
 ; TOPOLOGY: N/A
 ; MOLECULE TYPE: peptide
 ; ORIGINAL SOURCE:
 ; ORGANISM: N/A
 ; PUBLICATION INFORMATION:
 ; AUTHORS: N/A
 ; TITLE: N/A
 ; DOCUMENT NUMBER: PCT/US92/08069
 ; FILING DATE: 14-AUG-1993
 ; US-08-303-025-13

Query Match 33.8%; Score 72; DB 1; Length 29;
 Best Local Similarity 72.4%; Pred. No. 0.14; Mismatches 2; Indels 4; Gaps 2;

Qy 1 AKYAKKAK--AEKAKKAYKAAEAKKAAK 27
 ||| ||||| |:||||| |:|||||
 Db 2 AKKAAKKAKKAAKAAKKA--AKKAKKAAK 28

Search completed: June 3, 2005, 10:19:59
 Job time : 43 secs

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Best Local Similarity   41.7%; Pred. No. 2.2e+02;
Matches    15; Conservative      2; Mismatches    19; Indels      0; Gaps      0;

QY      10 AYAKKEKAQAEEKAYKAAEAKGAEAKYKAEAA 45
       ||| : ||| : ||| : ||| : ||| : ||| :
DB      19 AYAHKKDAKKPELSSQLVAHKDKKDAKKPKNSVA 54

RESULT 11
T07842
probable histone H1-3 - rape (fragment)
C:Species: Brassica napus (rape)
C>Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C:Accession: T07842
R:Deleu, C.; Coustaunt, M.; Niogret, M.F.; Larher, F.
submitted to the EMBL Data Library, January 1998
A:Reference number: Z16169
A:Accession: T07842
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-56 <DEL>
A:Cross-references: UNIPROT:O49175; EMBL:AF042182; NID:g2809203; PIDN:AAB97684.
A:Experimental source: cv. oleifera
C:Function:
A>Description: histone H3 plays a key role in nucleosome formation
C:Keywords: DNA binding; nucleosome

Query Match          19.2%; Score 51; DB 2; Length 56;
Best Local Similarity 35.1%; Pred. No. 3.3e+02;
Matches    13; Conservative      5; Mismatches    19; Indels      0; Gaps      0;

QY      2 KKYAKKEKAYKAAEKAAKKAAEKAYKAAEAOKKAAEA 38
       | : | : | : | : | : | : | : | : | : | :
DB     17 KTVSKPEMVTTKKRKAQPRQLKSIKSPGSKVLRA 53

RESULT 12
S58853
homeotic protein ultrabithorax homolog - Junonia coenia (fragment)
N:Alternate names: ultrabithorax homeodomain protein
C:Species: Junonia coenia
C>Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 16-Aug-2004
C:Accession: S58853
R:Warren, R.W.; Nagy, L.; Selegue, J.; Gates, J.; Carroll, S.
Nature 372, 458-461, 1994
A>Title: Evolution of homeotic gene regulation and function in flies and butterflies
A:Reference number: S58850; MUID:95075456; PMID:7840822
A:Accession: S58853
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-40 <WAR>
A:Cross-references: UNIPROT:Q25210; EMBL:L42137
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1995
C:Superfamily: homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match          18.8%; Score 50; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 3.1e+02;
Matches    14; Conservative      4; Mismatches    17; Indels      0; Gaps      0;

QY      21 KAENAKYAAEAKKKAEEKAYKAAEAKAAKAAEAYE 55
       ||| : ||| : ||| : ||| : ||| : ||| :
DB      2 KKEIQAIKELNEQEKAQAQAAAAAAAAD 36

RESULT 13
SI0263
histone H3.2 - Tetrahymena borealis (fragment)
C:Species: Tetrahymena borealis
C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C:Accession: SI0263
R:Brunk, C.F.; Kahn, R.W.; Sadler, L.A.
J. Mol. Evol. 30, 290-297, 1990

```


RESULT 15
T07242
hypothetical protein 49b - *Chlorella vulgaris* chloroplast
C/Species: chloroplast *Chlorella vulgaris*
C/Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C/Accession: T07242
R/Wakasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Tsudzuki, J.; Nakas
Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997
A/Ritle: Complete nucleotide sequence of the chloroplast genome from the green alga *Chlo*
A/Reference number: Z15985; MUID:97303241; PMID:9159184
A/Accession: T07242
A/Status: preliminary; translated from GB/EMBL/DBD
A/Molecule type: DNA
A/Residues: 1-49 <WAK>
A/Cross-references: EMBL:AB001684; NID:G2224352; PIDN:BAA57889.1; PID:G2224405
C/Genetics:
A/Genome: chloroplast

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	75	28.2	43	2	Q6MGW9	Q6mgw9 bdellovibri
2	68.5	25.8	45	1	PHI3 MYTCA	P11860 mytilus cal
3	68	25.6	44	2	Q71IY2	Q71iy2 lactobacill
4	64.5	24.2	42	2	Q9DF18	Q9df18 myxocephal
5	61	22.9	45	1	ANP8 MYOSC	P04368 myxocephal
6	60.5	22.7	51	2	Q7RF81	Q7rf81 plasmodium
7	59.5	22.4	53	1	MAR3 LEIMA	P14700 leishmania
8	59	22.2	35	2	Q747M3	Q747m3 geobacter s
9	57.5	21.6	37	2	Q74CW2	Q74cw2 geobacter s
10	56	21.1	40	1	ANP8 MYOAE	P20617 myxocephal
11	55.5	20.9	54	2	Q6F1A3	Q6fia3 mesoplasma
12	54.5	20.5	54	2	Q97314	Q97314 plasmodium
13	53	19.9	48	2	Q6L0J1	Q6l0j1 picrophilus
14	53	19.9	54	2	Q9ZK25	Q9zk25 helicobacte
15	52.5	19.7	51	2	Q9UMH6	Q9umh6 homo sapien
16	52.5	19.7	54	2	Q983T3	Q983t3 rhizobium l
17	51.5	19.4	49	1	SYSP CRIGR	Q781a2 cricetulus
18	51.5	19.4	55	2	Q88UN5	Q88un5 lactobacill
19	51	19.2	42	2	Q96RT9	Q96rt9 homo sapien
20	51	19.2	53	2	Q7YV63	Q7yv63 trypanosoma
21	51	19.2	56	2	Q49175	Q49175 brassica na
22	50	18.8	42	2	Q25210	Q25210 junonia coe
23	49	18.4	44	2	Q6RY82	Q6ry82 pongo pygma
24	49	18.4	44	2	Q6RY92	Q6ry92 pan troglod
25	49	18.4	44	2	Q6RY94	Q6ry94 macaca fasc
26	49	18.4	44	2	Q84ZD8	Q84zd8 oryza sativ
27	48	18.0	38	2	Q81TC9	Q81tc9 bacillus an
28	48	18.0	55	2	Q8N6F0	Q8n6f0 homo sapien
29	47.5	17.9	42	2	Q81P74	Q81p74 trypanosoma
30	47	17.7	31	3	DDSK PHYDS	P83638 phyllomedus
31	47	17.7	50	2	Q71IPI1	Q71ipi1 lactobacill

RP	SEQUENCE FROM N.A.
RX	TISSUE=Skin;
RC	MEDLINE=21192197; PubMed=11136728; DOI=10.1074/jbc.M009293200;
RA	Low W.-K., Lin Q., Stathakis C., Miao M.; Fletcher G.L., Hew C.L.;
RT	"Isolation and characterization of skin-type, type I antifreeze
RT	polypeptides from the longhorn sculpin, Myoxocephalus
RT	octodecemspinosus.";
RL	J. Biol. Chem. 276:11582-11589(2001).
RN	[2]
RP	SEQUENCE FROM N.A.
RX	TISSUE=Skin;
RC	Low W., Lin Q., Stathakis C., Miao M., Fletcher G.L., Hew C.L.;
RL	Submitted (SEP-2000) to the EMBL/GenBank/DDJJ databases.
DR	EMBL; AF306348; AAG22048.1 ; -
SQ	SEQUENCE 42 AA; 3796 MW; 73C566FE6G3AFB08 CRC64;
Query Match 24.2%; Score 64.5; DB 2; Length 42; Best Local Similarity 53.7%; Pred. No. 1.le+02; Matches 22; Conservative 1; Mismatches 17; Indels 1; Gaps 1;	
Qy	10 AVAKAEKAKKAAEKAYKAAEAKKGAAKYKAEAKAAAAA 50 : : Db 3 APAKAAKTADAKAAAATA-ADALAAANKTAAAKAAAK 42 : :
RESULT 5	
ANP8_MYOSC	STANDARD; PRT; 45 AA.
AC	P04358;
DT	20-MAR-1987 (Rel. 04, Created)
DT	20-MAR-1987 (Rel. 04, Last sequence update)
DT	05-JUL-2004 (Rel. 44, Last annotation update)
DE	Antifreeze peptide SS-8.
OS	Myxocephalus scorpius (Shorthorn sculpin) (daddy sculpin).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Actinopterygii; Neopterigiil; Teleostei; Euteleosteoi; Neoteleostei;
OC	Acanthomorpha; Acanthopterygiil; Percomorphia; Scorpaeniformes;
CC	Cottoidel; Cottidae; Myxocephalus.
OX	NCBI_TaxID=8097;
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=85285003; PubMed=4029130;
RA	Hew C.-L., Joshi S., Wang N.-C., Kao M.H., Anathanarayanan V.S.;
RT	*Structures of shorthorn sculpin antifreeze polypeptides.";
EL	Eur. J. Biochem. 151:167-172(1985).
CL	-I- FUNCTION: Antifreeze proteins lower the blood freezing point.
CC	-I- SIMILARITY: Belongs to the type-I AFP family. PIR; A05163; A05163. Direct protein sequencing; Repeat. KW Antifreeze protein; Blocked amino end (Met). FT MOD RES 1 1 FT REPEAT 9 21 FT REPEAT 22 33 FT REPEAT 34 45 SQ SEQUENCE 45 AA; 4006 MW; 26C0BCCG3B6878 CRC64;
Query Match 22.9%; Score 61; DB 1; Length 45; Best Local Similarity 47.4%; Pred. No. 2.2e+02; Matches 18; Conservative 4; Mismatches 16; Indels 0; Gaps 0;	
Qy	12 AKTAKEAKKAAEKAYKAAEAKKGAAKYKAEAKAAAA 49 : Db 7 AQQAARLLAAAAALAATAADAATAKAAKAAIAAAAAAS 44 :
RESULT 6	
Q7RF81	PRELIMINARY; PRT; 51 AA.
ID	Q7RF81;
AC	Q7RF81;
DT	01-MAR-2004 (TrEMBLrel. 26, Created)
DT	01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	Hypothenical protein.
GN	Name=PY04827;

FT	REPEAT	1	10		1.
FT	REPEAT	11	20		2.
FT	REPEAT	21	30		3.
FT	REPEAT	31	40		4.
FT	REPEAT	41	50		5.
FT	REPEAT	51	>53		6 (partial).
FT	NON_TER	53	53		
SQ	SEQUENCE	53 AA;	75D264BB078C06C6 CRC64;		
 Query Match 22.4%; Score 59.5; DB 1; Length 53; Best Local Similarity 40.9%; Pred. No. 3.4e+02; Matches 18; Conservative 13; Mismatches 10; Indels 3; Gaps 1;					
Qy	14 KAEEAKGAEEAKYKAAEAKKKAE--AKYKAAEAARAAKEAAYE 55				
Dd	11 EAEEAARQ-QAEAEAARLQAEEAARLQAEEAARLQAEEAARLQAEEA 53				
 RESULT 8					
Q747M3	ID Q747M3 PRELIMINARY; PRT; 35 AA.				
AC	Q747M3;				
DT	05-JUL-2004 (T-EMBLrel. 27, Created)				
DT	05-JUL-2004 (T-EMBLrel. 27, Last sequence update)				
DT	05-JUL-2004 (T-EMBLrel. 27, Last annotation update)				
DE	Hypothetical protein.				
GN	OrderedLocusNames=GSU3242;				
OS	Geobacter sulfurreducens.				
OC	Bacteria; Proteobacteria;				
OC	Geobacteriaceae; Geobacter.				
OX	NCBI_TaxID=35554;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=PCA / ATCC 51573;				
RX	PubMed=14671304; DOI=10.1126/science.1088727;				
RA	Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,				
RA	Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,				
RA	Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,				
RA	Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,				
RA	Davidsen T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,				
RA	Weidman J.F., Khouri H.M., Feldblum T.V., Utterback T.R.,				
RA	Van Aken S.E., Lovley D.R., Frazer C.M.;				
RT	"Genome of Geobacter sulfurreducens: metal reduction in subsurface				
RT	environments."				
RL	Science 302:1967-1969(2003) .				
DR	ENBL; AE017180; AAR36633.1; -.				
DR	TIGR; GSU3242; --				
SQ	Complete proteome; Hypothetical protein.				
KW	SEQUENCE 35 AA; 3966 MW; 0B6E2B600A034777 CRC64;				
 Query Match 22.2%; Score 59; DB 2; Length 35; Best Local Similarity 53.1%; Pred. No. 2.6e+02; Matches 17; Conservative 3; Mismatches 10; Indels 2; Gaps 1;					
Qy	6 KKPKAYAKKA-EA--AKKA-EAKYKAAEAKKK 35				
Dd	3 KEKKPVKKAKKAKKAKEKKKEEAAAAPAAEK 34				
 RESULT 9					
Q74CW2	ID Q74CW2 PRELIMINARY; PRT; 37 AA.				
AC	Q74CW2;				
DT	05-JUL-2004 (T-EMBLrel. 27, Created)				
DT	05-JUL-2004 (T-EMBLrel. 27, Last sequence update)				
DT	05-JUL-2004 (T-EMBLrel. 27, Last annotation update)				
DE	Hypothetical protein.				
GN	OrderedLocusNames=GSUI559;				
OS	Geobacter sulfurreducens.				
OC	Bacteria; Proteobacteria;				
OC	Geobacteriaceae; Geobacter.				
OX	NCBI_TaxID=35554;				
RN	[1]				

OC Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
OC Entomoplasmataceae; Mesoplasma.
OX NCBI_TaxID=2151;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=L1 / ATCC 33453;
RA Birren B.W., Strange-Thomann N., Hafez N., DeCaprio D., Fisher S.,
RA Butler J., Elkins T., Kodira C.D., Major J.C., Wang S., Nicol R.,
RA Nusbaum C.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AS017263; RAT75720.1; -;
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0005840; C:ribosome; IEA.
DR GO: GO:0003735; F:structural constituent of ribosome; IEA.
DR GO: GO:0006412; P:protein biosynthesis; IEA.
DR InterPro: IPR001911; Ribosomal_S21.
DR TIGRFAMs: TIGR00030; S21p; 1.
KW Complete proteome; Ribosomal protein.
KW Complete proteome; Ribosomal protein.
SQ SEQUENCE 54 AA; 6492 MW; A429E0AD37C39B95 CRC64;
Query Match 20.9%; Score 55.7; DB 2; Length 54;
Best Local Similarity 37.5%; Pred. No. 5; 3e+02;
Matches 15; Conservative 4; Mismatches 16; Indels 5; Gaps
QY 2 KYVAKKEKAYKAAKAAKAFKAYKAAEKKAAYK 41
: | | | | | | | | | | | | | | | | | | | |
DB 20 QKVASSNKAARKREYVLSKKEKRY-----KQKNRYK 54
: | | | | | | | | | | | | | | | | | | | |
RESULT 12
O97314 PRELIMINARY; PRT; 54 AA.
ID O97314
OC 097314;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DE Hypothetical protein MAL3P.36 (P49C12.11-like protein).
DE Name=MAL3P7.36; Synonyms=PFC1025;
OS Plasmodium falciparum (isolate 3D7).
GN Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP MEDLINE=99376085; PubMed=10448855; DOI=10.1038/22964;
RA Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,
RA Churcher C.M., Craig A., Davies R.M., Devlin K., Feltwell T.,
RA Gentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Hornsby T.,
RA Horrocks P., Jagels K., Jaesal B., Kyes S., McLean J., Moule S.,
RA Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A.,
RA Rutter S., Skelton J., Squares R., Squares S., Sulston J.E.,
RA Whitehead S., Woodward J.R., Newbold C., Barrell B.G.;
RT "The complete nucleotide sequence of chromosome 3 of Plasmodium
falciparum.";
RL Nature 400:532-538 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22255708; PubMed=12368867; DOI=10.1038/nature01095;
RA Hall N.K., Pain A., Berriman M., Churcher C., Harris B., Harris D.,
RA Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,
RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
RA Cronin A., Davies R., Davis P., Dear P., Dearden R., Doggett J.,
RA Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
RA Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
RA Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,
RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitsch E.,
RA Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
RA Sulston J.E., Craig A., Newbold C., Barrell B.G;
RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";


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RL Nature 419:527-531(2002).
DR EMBL; AL034559; CAB39063.1; -.
KW Hypothetical protein.
SQ SEQUENCE 54 AA; 6065 MW; E24DBCEB3DE2492B CRC64;

Query Match      20.5%; Score 54.5; DB 2; Length 54;
Best Local Similarity 44.4%; Pred. No. 8.8e+02;
Matches 20; Conservative 3; Mismatches 15; Indels 7; Gaps 2;

Qy 13 KKAEEAKA-----EAKYAAEA-KKKAAYKAAEAAXAAK 50
    ||||| | | | | | | | | | | | | | | | | | | |
Db 10 KKPLKAAKKGPVELTEEDIAFKEMAEEKKAAEEAKQKLLAKKK 54

RESULT 13
Q6LOJ1 ID Q6LOJ1 PRELIMINARY; PRT; 48 AA.
AC Q6LOJ1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=PTO0926;
OS Picrophilus torridus.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Picrophilaceae; Picrophilus.
OX NCBI_TaxID=82076;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 9790 / ATCC 700027;
RX PubMed=15184674; DOI=10.1073/pnas.0401356101;
RA Fuetterer O., Angelov A., Liesegang H., Gottschalk G., Schleper C.,
RA Schepers B., Dock C., Antranikian G., Liebl W.;
RT "Genome sequence of Picrophilus torridus and its implications for life
RT around pH 0.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9091-9096(2004).
DR EMBL; AE017261; AAT43511.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 48 AA; 5394 MW; A08C0B68E9FA99D5 CRC64;

Query Match      19.9%; Score 53; DB 2; Length 48;
Best Local Similarity 40.0%; Pred. No. 1.1e+03;
Matches 14; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

Qy 2 KKYAKGEKAYAKAEKAAKKAAYKAAEAAYKKA 36
    | : | | | | | | | | | | | | | | | |
Db 4 KEDKKKEFLKLRKNSIKSDDTAEDAAAEEDA 38

RESULT 14
Q9ZK25 ID Q9ZK25 PRELIMINARY; PRT; 54 AA.
AC Q9ZK25;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative motility protein.
GN OrderedLocusNames=JHP117;
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682; DOI=10.1038/16495;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
```

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DR EMBL; AE001539; AAD06698.1; -.
DR PIR; F71847; F71847.
KW Complete proteome.
SQ SEQUENCE 54 AA; 5873 MW; 96C37ACAB155C35C CRC64;

Query Match      19.9%; Score 53; DB 2; Length 54;
Best Local Similarity 41.7%; Pred. No. 1.2e+03;
Matches 15; Conservative 2; Mismatches 19; Indels 0; Gaps 0;

Qy 10 AYAKKAEEAKKAAYKAAEAAYKAAEAAYKAAEAAYKAAEA 45
    ||||| | | | | | | | | | | | | | | | |
Db 19 AYAHKDKDAKKPELSSQLVAHKDKDAKKPKNSVA 54

RESULT 15
Q9UMH6 ID Q9UMH6 PRELIMINARY; PRT; 51 AA.
AC Q9UMH6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SS-B/La protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90237237; PubMed=1692037;
RA Kohesaka H., Yamamoto K., Fujii H., Miura H., Miyasaka N., Nishio K.,
RA Miyamoto T.;
RT "Fine epitope mapping the human SS-B/La protein: Identification of a
RT distinct autoepitope homologous to a viral gag polyprotein.";
RL J. Clin. Invest. 85:1566-1574(1990).
DR EMBL; M35263; AAA36653.1; -.
FT NON_TER 1
FT NON_TER 51
SQ SEQUENCE 51 AA; 6218 MW; EA152B8386E7F078 CRC64;

Query Match      19.7%; Score 52.5; DB 2; Length 51;
Best Local Similarity 42.1%; Pred. No. 1.2e+03;
Matches 16; Conservative 5; Mismatches 12; Indels 5; Gaps 2;

Qy 7 KEKAYAK-AEKAANKAEKAAEAAYKAAEAAYKAAEAAYKAE 43
    | : | | | | | | | | | | | | | | | |
Db 12 KDDYFAKKNEERKONKVEAK----LRKQEQEAKQKLE 45

Search completed: June 3, 2005, 10:34:25
Job time : 173 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2005, 10:20:03 ; Search time 157 Seconds
(without alignments)
137.953 Million cell updates/sec

Title: US-10-792-311-3

Perfect score: 266

Sequence: 1 AKYAKKEKAYAKAEKAAK.....EAKYKAERAAKAAKEAAAYEA 56

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 974573

Minimum DB seq length: 0

Maximum DB seq length: 56

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	266	100.0	56	3 AAY82573	Aay82573 Copolymer
2	134.5	50.6	45	3 AAY82572	Aay82572 Copolymer
3	104.5	39.3	35	3 AAY82571	Aay82571 Copolymer
4	93.5	35.2	46	2 AAW24449	Aaw24449 Nucleic a
5	89.5	33.6	46	2 AAR28871	Aar28871 High affi
6	88.5	33.3	56	8 ADO43176	Ado43176 Peptide u
7	84	31.6	32	2 AAR90180	Aar90180 Polycatio
8	84	31.6	32	2 AAW06686	Aaw06686 Protamine
9	84	31.6	33	2 AAR90181	Aar90181 Polycatio
10	84	31.6	33	2 AAW06688	Aaw06688 Protamine
11	82.5	31.0	40	3 AAB08170	Aab08170 Peptide m
12	82.5	31.0	49	8 ADO43172	Ado43172 Peptide u
13	79.5	29.9	29	2 AAR90179	Aar90179 Polycatio
14	79.5	29.9	29	2 AAW06698	Aaw06698 Protamine
15	79	29.7	29	2 AAR90178	Aar90178 Polycatio
16	79	29.7	29	2 AAR90176	Aar90176 Polycatio
17	79	29.7	29	2 AAW06687	Aaw06687 Protamine
18	79	29.7	29	2 AAW06697	Aaw06697 Protamine
19	76.5	28.8	55	2 AAY34069	Aay34069 Histone H
20	76.5	28.8	55	2 AAY57367	Aay57367 Human his
21	75.5	28.4	36	3 AAB08169	Aab08169 Peptide m
22	75	28.2	56	8 ADO43179	Ado43179 Peptide u
23	74	27.8	28	2 AAR90177	Aar90177 Polycatio
24	74	27.8	28	2 AAW06685	Aaw06685 Protamine
25	74	27.8	37	2 AAR74719	Aar74719 Tryptic d

26	74	27.8	37	2 AAR64798	Aar64798 Amphipath
27	74	27.8	37	2 AAR77070	Aar77070 Synthetic
28	74	27.8	37	2 AAR92400	Aar92400 Lytic pep
29	74	27.8	37	2 AAR90754	Aar90754 Synthetic
30	74	27.8	37	2 AAW39771	Aaw39771 Synthetic
31	72	27.1	37	2 AAW08401	Aaw08401 Nucleic a
32	72	27.1	37	2 AAW69205	Aaw69205 Nucleic a
33	72	27.1	39	2 AAW44934	Aaw44934 Mycobacte
34	72	27.1	39	7 ADF45561	Adf45561 Methylate
35	72	27.1	40	2 AAW38814	Aaw38814 Delivery
36	72	27.1	41	2 AAW38815	Aaw38815 Delivery
37	72	27.1	42	2 AAW38816	Aaw38816 Delivery
38	72	27.1	42	8 ADO43175	Ado43175 Peptide u
39	72	27.1	43	2 AAW38817	Aaw38817 Delivery
40	72	27.1	45	2 AAW24450	Aaw24450 Nucleic a
41	72	27.1	45	3 AAY98493	Aay98493 Peptide #
42	72	27.1	45	3 AAY59038	Aay59038 Peptide u
43	72	27.1	45	4 AAB45846	Aab45846 Nucleic a
44	72	27.1	45	4 AAU04283	Aau04283 Trimeric
45	71.5	26.9	53	4 AAU18248	Aau18248 Novel hum

ALIGNMENTS

RESULT 1

AAy82573

ID AAY82573 standard; peptide; 56 AA.

XX AC AAY82573;

DT 28-JUL-2000 (first entry)

DE DE Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:3.

KW Copolymer; molecular weight marker; TV-marker; immune disease;

KW glutaric acetate; autoimmune disease; antiarthritic; neuroprotective;

KW osteopathic; immunosuppressive; antithyroid; antiinflammatory;

KW antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological;

KW antianemic; immunosuppressive; demyelinating disease; osteoarthritis;

KW inflammatory condition; multiple sclerosis; rheumatoid arthritis;

KW Crohn's disease; chronic immune thrombocytopenia purpura; colitis;

KW diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis;

KW Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;

KW pemphigus vulgaris; systemic lupus erythematosus.

XX OS Unidentified.

XX FN WO200018794-A1.

XX PD 06-APR-2000.

XX PF 24-SEP-1999; 99WO-US022402.

XX PR 25-SEP-1998; 98US-0101693P.

XX PA (YEDA) YEDA RES & DEV CO LTD.

XX PA (TEVA-) TEVA PHARM USA INC.

XX PI Gad A, Lis D;

XX XX WPI; 2000-317499/27.

XX Copolymer 1 related polypeptides used as molecular weight markers for
glutaric acetate and for treatment and prevention of immune diseases.

XX Claim 10; Page 14; 72pp; English.

XX AAY82571 to AAY82577 represent specifically claimed copolymer molecular
weight TV-marker polypeptides from the present invention. The present
invention describes polypeptides (I) for determining the molecular weight
of a copolymer (CP), which has an identified molecular weight and an
amino acid composition corresponding to the copolymer. The polypeptides

RESULT 2	
AA82572	
ID	AA892572 standard; peptide; 45 AA.
XX	
AC	AA82572;
XX	
DT	28-JUL-2000 (first entry)
XX	
DE	Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:2.
XX	
KW	Copolymer; molecular weight marker; TV-marker; immune disease;
KW	glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective;
KW	osteopathic; immunosuppressive; antithyroid; antiinflammatory;
KW	antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological;
KW	antianaemic; immunosuppressive; demyelinating disease; osteoarthritis;
KW	inflammatory condition; multiple sclerosis; rheumatoid arthritis;
KW	Crohn's disease; chronic immune thrombocytopaenia purpura; colitis;
KW	diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis;
KW	Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
KW	pemphigus vulgaris; systemic lupus erythematosus.
XX	
OS	Unidentified.
XX	
PN	WO200018794-A1.
XX	
PD	06-APR-2000.
XX	
PF	24-SEP-1999; .. 99WO-US022402.
XX	
PR	25-SEP-1998; 98US-0101693P.
XX	
PA	(YEDA) YEDA RES & DEV CO LTD.
PA	(TEVA-) TEVA PHARM USA INC.
XX	
PI	Gad A, Lis D;
XX	
DR	WPI; 2000-317499/27.
XX	
PT	Copolymer 1 related polypeptides used as molecular weight markers for
PT	glatiramer acetate and for treatment and prevention of immune diseases.
XX	
PS	Claim 10; Page 14; 72pp; English.
XX	
CC	AA82571 to AA82577 represent specifically claimed copolymer molecular


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Query Match      35.2%; Score 93.5; DB 2; Length 46;
Best Local Similarity 60.5%; Pred. No. 0.045;
Matches 26; Conservative 4; Mismatches 12; Indels 1; Gaps 1
Qy 9 KAVAKAEKAAKAEAKAYKAAAEAKCKAEAKYKAEAKAAK 50
    |||||
Db 2 KAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAK 44
    |||||

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XX	AK220711,
XX	
DT	25-MAR-2003 (revised)
DT	23-MAR-1993 (first entry)
DT	
XX	
XX	
DE	High affinity macrophage mannose receptor ligand compound #9.

glycopeptide; mannose; mannosylated; glycosylated; mannose receptor;
macrophages; monocytes; antigen; cytotoxicity; label; image; alter;
macrophage processing of antigen; MHC restriction; inflammation;

- KW lysosomal storage diseases; Gaucher's disease; asthma;
- KW alveolar macrophages metastasis; systemic macrophages; deliver;
- KW antigenic peptides; prevent transplant rejection; organ transplantation;

XX
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Synthetic.

OS
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antitumour agents; cancer; toxins.

FT	Modified-site	1	4
FT		/note= "opt may have mannose, fucose, glucose or N-Ac-glucosamine. May also have non interfering subsits."	
FT	Modified-site		

FT
glucosamine."

/note= "opt may have mannose, fucose, glucose or N-Ac-

FT	Modified-site	10

FT
glucosamine."

FTIR: 3400 (broad, O-H stretch), 2900 (C-H stretch), 1735 (C=O stretch, aldehyde), 1600 (C=C stretch, aromatic), 1510 (C=C stretch, aromatic), 1450 (C-O stretch), 1380 (C-O stretch), 1270 (C-O stretch), 1100 (C-O stretch), 1050 (C-O stretch), 1010 (C-O stretch), 960 (C=C stretch, aromatic), 910 (C=C stretch, aromatic), 830 (C-H bend, aromatic), 750 (C-H bend, aromatic), 700 (C-H bend, aromatic), 690 (C-H bend, aromatic), 600 (C-H bend, aromatic).

FT	Modified-site	glucosamine:
16		16

ET may have mannose, glucose or fructose residues.
glucosamine."

FI	MODIFIED-SITE	IS	/note= "opt may have mannose, fucose, glucose or N-Ac-
FT			

FT	Modified-site	FT
22	glucosamine.	
	/note= "opt may have mannose, fucose, glucose or N-Ac-	

PT	Modified-site	gracuuming: 25
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FT Modified-site 28

XX New poly:cationic polypeptide n-protamine analogues - having reduced
 PT cationic charge and lower toxicity, used for reversing (low mol.wt.)
 PT heparin anticoagulation.
 XX
 PS Disclosure; Page 13; 34pp; English.
 XX
 CC Novel peptides are claimed which contain 20-40 amino acids and which have
 CC a total cationic charge of less than +21 (pref. +16 to +18; esp. +18) as
 CC determined by the number of positively charged amino acids in the
 CC sequence. Preferably the positive charges are grouped in clusters
 CC separated by neutral amino acids. Especially the peptides contain 28-32
 CC amino acids having blocks of 2-4 positively charged amino acids separated
 CC by blocks of 2-6 neutral acids. Alternatively the positive charge may be
 CC distributed evenly or randomly along the peptide sequence. In particular
 CC the peptides are analogues of n-protamine (total cationic charge = +21)
 CC in which selected arginine residues have been replaced with uncharged
 CC amino acids and other arginine residues have been replaced by other
 CC positively charged amino acid residues, preferably lysine. The peptides
 CC reverse the effect of low mol. wt. heparin (LMWH) anticoagulation and
 CC hence can be used medically to prevent bleeding after the conclusion of
 CC clinical procedures using heparin therapy. They are less toxic than n-
 CC protamine since the reduced positive charge gives an improved efficiency
 CC to toxicity ratio; and they may be more effective than n-protamine in
 CC their anti-LMWH action. The present sequence (total cationic charge =
 CC +18) is a specific example of the new polypeptides
 XX
 SQ Sequence 29 AA;

Query Match 29.9%; Score 79.5; DB 2; Length 29;
 Best Local Similarity 69.0%; Pred. No. 0.25;
 Matches 20; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

Qy 7 KEKAYAKKAEKAKKAEKAKYKAAEAKKK 35
 Db 2 KKGA-AKKAKKAAKAKKAAKAKKAKKK 29

RESULT 14
 AAW06698
 ID AAW06698 standard; peptide; 29 AA.
 XX
 AC AAW06698;
 XX
 DT 06-AUG-1997 (first entry)
 XX
 DE Protamine-like peptide analogue PK(K2A2K2A)3K2AK3 with charge [+18].
 XX
 KW Coagulation; anticoagulant; heparin; platelet aggregation; cell adhesion;
 KW positively charged cluster; arginine; polycationic; decrease;
 KW n-protamine; salmine protamine; protamine sulphate; salmon sperm.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 3. .23
 FT /label= repeat region
 FT /note= "3 tandem repeats of (Lys)2(Ala)2(Lys)2Ala motif"
 XX
 PN W09635444-A1.
 XX
 PD 14-NOV-1996.
 XX
 XX 08-MAY-1996; 96WO-US006567.
 PF
 XX 08-MAY-1995; 95US-00436703.
 PR
 XX (UNMI) UNIV MICHIGAN.
 PA
 XX Wakefield TW, Stanley JC, Andrews PC;
 PI
 XX WPI; 1997-011697/01.
 DR
 XX

PT Peptide reversing the anticoagulant effects of heparin - is based on
 PT protamine but has fewer positive charges for reduced toxicity.
 XX
 PS Disclosure; Page 13; 42pp; English.
 XX
 CC Protamine sulphate (also called n-protamine or salmine protamine) is a
 CC polycationic peptide derived from salmon sperm and is used to reverse
 CC heparin anticoagulation. One of the major components of salmine protamine
 CC is a 32 amino acid peptide having a total cationic charge of [+21], with
 CC arginine accounting for 67% of the total sequence and for all of the
 CC positive charge. Peptides of 20-40 amino acids with total cationic charge
 CC less than [+21] and which are able, at least partially, to reverse the
 CC effect of heparin and/or low molecular weight heparin anticoagulants are
 CC claimed. Specifically, the peptides are polycationic analogues of n-
 CC protamine where the positive charge on the amino acid sequence is reduced
 CC by selective replacement of positively charged arginine residues with an
 CC uncharged residue, so that total cationic charge is less than [+21]. The
 CC new peptides are used in vivo to reverse the effects of heparin; they
 CC have the same anti-heparin activity as protamine but are less toxic
 CC (because of the reduced number of positive charges) and are relatively
 CC easy and inexpensive to prepare. The present sequence represents a
 CC specific example of a protamine-like peptide with a charge of [+18] which
 CC has been found to reverse the anticoagulation effects of both standard
 CC and low molecular weight heparin
 XX
 SQ Sequence 29 AA;

Query Match 29.9%; Score 79.5; DB 2; Length 29;
 Best Local Similarity 69.0%; Pred. No. 0.25;
 Matches 20; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

Qy 7 KEKAYAKKAEKAKKAEKAKYKAAEAKKK 35
 Db 2 KKGA-AKKAKKAAKAKKAAKAKKAKKK 29

RESULT 15
 AAR90178
 ID AAR90178 standard; peptide; 29 AA.
 XX
 AC AAR90178;
 XX
 DT 25-MAR-1996 (first entry)
 XX
 DE Polycationic polypeptide n-protamine analogue.
 XX
 KW n-protamine; anticoagulation reversal; low molecular weight heparin;
 KW polycationic; positively charged amino acid; lysine.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "N-terminal is acetylated"
 FT Modified-site 29
 FT /note= "C-terminal is in amide form"
 XX
 PN W09513083-A1.
 XX
 PD 18-MAY-1995.
 XX
 XX 10-NOV-1994; 94WO-US012981.
 PF
 XX 12-NOV-1993; 93US-00152488.
 PR
 XX 08-SEP-1994; 94US-00303025.
 PR
 XX (UNMI) UNIV MICHIGAN.
 PA
 XX Wakefield TW, Stanley JC, Andrews PC;
 PI
 XX WPI; 1995-193899/25.
 DR
 XX New poly:cationic polypeptide n-protamine analogues - having reduced
 PT

PT cationic charge and lower toxicity, used for reversing (low mol.wt.)
XX heparin anticoagulation.
PS Disclosure; Page 13; 34pp; English.
XX
CC Novel peptides are claimed which contain 20-40 amino acids and which have
CC a total cationic charge of less than +21 (pref. +16 to +18; esp. +18) as
CC determined by the number of positively charged amino acids in the
CC sequence. Preferably the positive charges are grouped in clusters
CC separated by neutral amino acids. Especially the peptides contain 28-32
CC amino acids having blocks of 2-4 positively charged amino acids separated
CC by blocks of 2-6 neutral acids. Alternatively the positive charge may be
CC distributed evenly or randomly along the peptide sequence. In particular
CC the peptides are analogues of n-protamine (total cationic charge = +21)
CC in which selected arginine residues have been replaced with uncharged
CC amino acids and other arginine residues have been replaced by other
CC positively charged amino acid residues, preferably lysine. The peptides
CC reverse the effect of low mol. wt. heparin (LMWH) anticoagulation and
CC hence can be used medically to prevent bleeding after the conclusion of
CC clinical procedures using heparin therapy. They are less toxic than n-
CC protamine since the reduced positive charge gives an improved efficiency
CC to toxicity ratio; and they may be more effective than n-protamine in
CC their anti-LMWH action. The present sequence (total cationic charge =
CC +16) is a specific example of the new polypeptides
XX
SQ Sequence 29 AA;
Query Match 29.7%; Score 79; DB 2; Length 29;
Best Local Similarity 67.9%; Pred. No. 0.28;
Matches 19; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
Qy 1 AKYAKKEKAYAKAEKAAKAEKAYK 28
| | | | | : | | | | | : | |
Db 2 AKAAKAKAKAAKAAKAAKAAKAAK 29
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Job time : 158 secs

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/ GENERAL INFORMATION:
/ APPLICANT: Braun, Jonathan
/ TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
/ Ulcerative Colitis, and Clinical Subtypes Thereof, Using
/ Microbial UC pANCA antigens
/ NUMBER OF SEQUENCES: 41
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Campbell & Flores LLP
/ STREET: 4370 La Jolla Village Drive, Suite 700
/ CITY: San Diego
/ STATE: California
/ COUNTRY: USA
/ ZIP: 92122
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA: US/10/229,567
/ FILING DATE: 27-Aug-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/417,264
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: US 09/041,889
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Campbell, Cathryn A.
/ REGISTRATION NUMBER: 31,815
/ REFERENCE/DOCKET NUMBER: P-PM 3006
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619) 535-9001
/ TELEFAX: (619) 535-8949
/ INFORMATION FOR SEQ ID NO: 41:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 55 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 41:
/
/ US-10-229-567-41
/
/ Query Match 28.8%; Score 76.5; DB 14; Length 55;
/ Best Local Similarity 48.1%; Pred. No. 1.6;
/ Matches 26; Conservative 4; Mismatches 19; Indels 5; Gaps 2;
/
/ QY 3 KYAKKEKAVA--KQAEKAAKAAE---KAYKAAEAKKKAEKYKAPAAKAAK 51
/ DB 1 KSPKKAAAKPKKATKSPAKPKAVKPKAAKPKAAKPKAAKPKAAKPKAAK 54
/
/ RESULT 9
/ US-10-424-599-177669
/ Sequence 177669, Application US/10424599
/ Publication No. US20040031072A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa Thomas J
/ APPLICANT: Kovalic David K
/ APPLICANT: Zhou Yihua
/ APPLICANT: Cao Yongwei
/ TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53223)B
/ CURRENT APPLICATION NUMBER: US/10/424,599
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 285684
/ SEQ ID NO 177669
/ LENGTH: 55
/ TYPE: PRT
/ ORGANISM: Glycine max
/ FEATURE:

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; OTHER INFORMATION: Clone ID: PAT_MRT3847_131450C.1.pap
US-10-424-599-177669

Query Match 28.6%; Score 76; DB 15; Length 55;
Best Local Similarity 40.0%; Pred. No. 1.8; Mismatches 20; Indels 0; Gaps 0;
Matches 18; Conservative 7

Qy 2 KKYAKKEKAYAKAEKAEKAEKAYKAAEAKKAEAKKAEAKYKAEAK 46
Db 1 RKNKK 45

RESULT 10

US-10-767-701-50521
; Sequence 50521, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 50521
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3480-013-P1-K1-E10.pap
US-10-767-701-50521

Query Match 28.2%; Score 75; DB 16; Length 53;
Best Local Similarity 42.2%; Pred. No. 2.1; Mismatches 21; Indels 0; Gaps 0;
Matches 19; Conservative 5

Qy 2 KKYAKKEKAYAKAEKAEKAEKAYKAAEAKKAEAKKAEAKYKAEAK 46
Db 2 KKK 46

RESULT 11

US-10-667-004-23
; Sequence 23, Application US/10667004
; Publication No. US20040126820A1
; GENERAL INFORMATION:
; APPLICANT: INTEL CORPORATION
; APPLICANT: CHAN, Selena
; APPLICANT: SU, Xing
; APPLICANT: YAMAKAWA, Mineo
; TITLE OF INVENTION: CONTROLLED ALIGNMENT OF NANO-BARCODES ENCODING SPECIFIC INFORMATION
; TITLE OF INVENTION: SCANNING PROBE MICROSCOPY (SPM)
; FILE REFERENCE: INTEL1310-1(P14240X)
; CURRENT APPLICATION NUMBER: US/10/667,004
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US 10/251,152
; PRIOR FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 23
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-667-004-23

Query Match 28.2%; Score 75; DB 16; Length 56;
Best Local Similarity 48.1%; Pred. No. 2.2; Mismatches 26; Indels 0; Gaps 0;
Matches 25; Conservative 1

Qy 5 AKKEKAYAKAEKAEKAEKAYKAAEAKKAEAKKAEAKYKAEAK 56
Db 3 AAAE 54

RESULT 12

US-10-424-599-182752
; Sequence 182752, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 182752
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_136039C.1.pap
US-10-424-599-182752

Query Match 27.4%; Score 73; DB 15; Length 51;
Best Local Similarity 42.2%; Pred. No. 3.2; Mismatches 21; Indels 0; Gaps 0;
Matches 19; Conservative 5

Qy 2 KKYAKKEKAYAKAEKAEKAEKAYKAAEAKKAEAKKAEAKYKAEAK 46
Db 5 KKK 49

RESULT 13

US-10-424-599-240336
; Sequence 240336, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 240336
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_59050C.1.pap
US-10-424-599-240336

Query Match 27.4%; Score 73; DB 15; Length 53;
Best Local Similarity 38.0%; Pred. No. 3.3; Mismatches 24; Indels 0; Gaps 0;
Matches 19; Conservative 7

Qy 2 KKYAKKEKAYAKAEKAEKAEKAYKAAEAKKAEAKKAEAKYKAEAK 51
Db 1 KKK 50

RESULT 14

US-10-424-599-247907
; Sequence 247907, Application US/10424599
; Publication No. US20040031072A1


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; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 247907
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_65891C.1.pep
US-10-424-599-247907
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Query Match 27.4%; Score 73; DB 15; Length 53;
Best Local Similarity 45.0%; Pred. No. 3.3;
Matches 18; Conservative 4; Mismatches 18; Indels 0; Gaps 0;
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Qy 2 KKYAKKKKAYAKKAAKAAKAYKAAEAKKAAKAAK 41
Db 10 KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK 49
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RESULT 15
US-10-437-963-138732
; Sequence 138732, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 138732
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_40093C.1.pep
US-10-437-963-138732
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Query Match 27.4%; Score 73; DB 16; Length 54;
Best Local Similarity 45.0%; Pred. No. 3.4;
Matches 18; Conservative 4; Mismatches 18; Indels 0; Gaps 0;
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Qy 2 KKYAKKKKAYAKKAAKAAKAYKAAEAKKAAKAAK 41
Db 4 KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK 43
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Search completed: June 3, 2005, 10:50:08
Job time : 138 secs
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10	84	31.6	32	1	US-08-303-025-15	Sequence 15, Appli
11	84	31.6	32	1	US-08-677-304-13	Sequence 13, Appli
12	84	31.6	32	2	US-08-436-703B-2	Sequence 2, Appli
13	84	31.6	33	2	US-08-303-025-16	Sequence 16, Appli
14	84	31.6	33	2	US-08-436-703B-4	Sequence 4, Appli
15	79.5	29.9	29	1	US-08-152-488-12	Sequence 12, Appli
16	79.5	29.9	29	1	US-08-303-025-14	Sequence 14, Appli
17	79.5	29.9	29	1	US-08-677-304-12	Sequence 12, Appli
18	79.5	29.9	29	2	US-08-436-703B-16	Sequence 16, Appli
19	79	29.7	29	1	US-08-152-488-10	Sequence 10, Appli
20	79	29.7	29	1	US-08-152-488-11	Sequence 11, Appli
21	79	29.7	29	1	US-08-303-025-10	Sequence 10, Appli
22	79	29.7	29	1	US-08-303-025-11	Sequence 11, Appli
23	79	29.7	29	1	US-08-303-025-13	Sequence 13, Appli
24	79	29.7	29	1	US-08-677-304-10	Sequence 10, Appli
25	79	29.7	29	1	US-08-677-304-11	Sequence 11, Appli
26	79	29.7	29	2	US-08-436-703B-3	Sequence 3, Appli
27	79	29.7	29	2	US-08-436-703B-15	Sequence 15, Appli

BEST LOCAL SIMILARITY 68.4%; FREQ. NO. 3.3E-07;

[illegible]


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; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: N/A
; TOPOLOGY: N/A
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: N/A
; PUBLICATION INFORMATION:
; AUTHORS: N/A
; TITLE: N/A
; DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
; US-08-303-025-15

Query Match 31.6%; Score 84; DB 1; Length 32;
Best Local Similarity 62.9%; Pred. No. 0.028;
Matches 22; Conservative 3; Mismatches 6; Indels

Qy 1 AKKYAKKKKAYAKKAKKAAKAKYAKYAKK 35
Db 2 AKKAAKKAKKAAKAKKAAKAKKAKKAKK 32

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RESULT 11
US-08-677-304-13
; Sequence 13, Application US/08677304
: Patent No 5721212

/ GENERAL INFORMATION:
 / APPLICANT: Wakefield, Thomas W.
 / APPLICANT: Andrews, Philip C.
 / APPLICANT: Stanley, James C.
 / TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
 / TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
 / TITLE OF INVENTION: ANTICOAGULATION REVERSAL
 / NUMBER OF SEQUENCES: 13

TITLE OF INVENTION: NOVEL FERTILIZERS FOR HEMP
 FIELD OF INVENTION: LOW MOLECULAR WEIGHT HEMP
 TITLE OF INVENTION: ANTICOAGULATION REVERSAL
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Benita J. Rohm, Esq.
 STREET: 512 Springfield Avenue
 CITY: Cranford
 STATE: New Jersey
 COUNTRY: United States of America
 ZIP: 07016-1811
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WordPerfect 6; ASCII (DOS) Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/677,304
 FILING DATE:
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/152,498
 FILING DATE: 12-NOV-1993
 APPLICATION NUMBER: FCT/US92/08069
 FILING DATE: 14-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Rohm, Benita J.
 REGISTRATION NUMBER: 28,664
 REFERENCE/POCKET NUMBER: RM-7WG
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 908-276-3344
 TELEFAX: 908-276-5543
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 32 amino acids
 TYPE: amino acid
 STRANDEDNESS: No. 5721212 Relevant
 TOPOLOGY: No. 5721212 Relevant
 MOLECULE TYPE: peptide
 ORIGINAL SOURCE:
 ORGANISM: N/A

PUBLICATION INFORMATION:

AUTHORS: N/A

TITLE: N/A

PUBLICATION INFORMATION:

DOCUMENT NUMBER: PCT/US92/08069

FILING DATE: 14-AUG-1993

US-08-677-304-13

Query Match 31.6%; Score 84; DB 1; Length 32;
Best Local Similarity 62.9%; Pred. No. 0.028;
Matches 22; Conservative 3; Mismatches 6; Indels 1;

Qy 1 AKKYAKKEKAYAKAEKAKAEKAYKAAEAKKK 35
Db 2 AKKAACKAKKAAKKAACKAKKAKKAKKAKKAKK 32

RESULT 12

US-08-436-703B-2

Sequence 2, Application US/08436703B

Patent No. 5919761

GENERAL INFORMATION:

APPLICANT: Wakefield, Thomas W.

APPLICANT: Andrews, Philip C.

APPLICANT: Stanley, James C.

TITLE OF INVENTION: NOVEL PEPTIDES FOR

TITLE OF INVENTION: HEPARIN AND LOW MOLECULAR

TITLE OF INVENTION: WEIGHT HEPARIN

TITLE OF INVENTION: ANTICOAGULATION REVERSAL

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Benita J, Rohm, Esq.

STREET: 6601 Woodward Avenue

STREET: Suite 1525

CITY: Detroit

STATE: Michigan

COUNTRY: United States of America

ZIP: 48226

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk 1.44Mb, 3.5"

COMPUTER: IBM PC compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 6;

SOFTWARE: ASCII (DOS)Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/436.703B

FILING DATE: 08-MAY-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: N/A

FILING DATE: N/A

ATTORNEY/AGENT INFORMATION:

NAME: Rohm, Benita J.

REGISTRATION NUMBER: 28,664

REFERENCE/DOCKET NUMBER: 7WK-060548-00233

TELECOMMUNICATION INFORMATION:

TELEPHONE: 313-965-1976

TELEFAX: 313-965-1951

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 32 amino acids

TYPE: amino acid

STRANDEDNESS: N/A

TOPOLOGY: N/A

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: N/A

PUBLICATION INFORMATION:

AUTHORS: N/A

TITLE: N/A

US-08-436-703B-2

Query Match

31.6%; Score 84; DB 2; Length 32;

Best Local Similarity 62.9%; Pred. No. 0.028;
Matches 22; Conservative 3; Mismatches 6; Indels 1;
Gaps 1;

Qy 1 AKKYAKKEKAYAKAEKAKAEKAYKAAEAKKK 35
Db 2 AKKAACKAKKAAKKAACKAKKAKKAKKAKKAKK 32

RESULT 13

US-08-303-025-16

Sequence 16, Application US/08303025

Patent No. 5614494

GENERAL INFORMATION:

APPLICANT: Wakefield, Thomas W.

APPLICANT: Andrews, Philip C.

APPLICANT: Stanley, James C.

TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND

TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN

TITLE OF INVENTION: ANTICOAGULATION REVERSAL

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Benita J, Rohm, Esq.

STREET: 150 West Jefferson, Suite 2500

CITY: Detroit

STATE: Michigan

COUNTRY: United States of America

ZIP: 48226-4415

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy diskette 3.5" 1.44Mb

COMPUTER: IBM PC compatible

OPERATING SYSTEM: MS-DOS v.6.22

SOFTWARE: WordPerfect 6.1; ASCII (DOS)Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/303,025

FILING DATE: 08-SEPT-1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/06829

FILING DATE: 14-AUG-1992

APPLICATION NUMBER: US 08/152,488

FILING DATE: 12-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: Rohm, Benita J.

REFERENCE/DOCKET NUMBER: 7WK-060548-00231

TELECOMMUNICATION INFORMATION:

TELEPHONE: 313-496-7622

TELEFAX: 313-496-8454

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 33 amino acids

TYPE: amino acid

STRANDEDNESS: N/A

TOPOLOGY: N/A

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: N/A

PUBLICATION INFORMATION:

AUTHORS: N/A

TITLE: N/A

DOCUMENT NUMBER: PCT/US92/08069

FILING DATE: 14-AUG-1993

US-08-303-025-16

Query Match

31.6%; Score 84; DB 1; Length 33;

Best Local Similarity 62.9%; Pred. No. 0.029;

Matches 22; Conservative 3; Mismatches 6; Indels 1;

Gaps 1;

Qy 1 AKKYAKKEKAYAKAEKAKAEKAYKAAEAKKK 35
Db 3 AKKAACKAKKAAKKAACKAKKAKKAKKAKKAKK 33

RESULT 14

US-08-436-703B-4
; Sequence 4, Application US/08436703B
; Patent No. 5919761
; GENERAL INFORMATION:
; APPLICANT: Wakefield, Thomas W.
; APPLICANT: Andrews, Philip C.
; APPLICANT: Stanley, James C.
; TITLE OF INVENTION: NOVEL PEPTIDES FOR
; TITLE OF INVENTION: HEPARIN AND LOW MOLECULAR
; TITLE OF INVENTION: WEIGHT HEPARIN
; TITLE OF INVENTION: ANTICOAGULATION REVERSAL
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Benita J. Rohm, Esq.
; STREET: 6601 Woodward Avenue
; STREET: Suite 1525
; CITY: Detroit
; STATE: Michigan
; COUNTRY: United States of America
; ZIP: 48226
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk 1.44Mb, 3.5"
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6;
; SOFTWARE: ASCII (DOS)Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,703B
; FILING DATE: 08-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: N/A
; FILING DATE: N/A
; ATTORNEY/AGENT INFORMATION:
; NAME: Rohm, Benita J.
; REGISTRATION NUMBER: 28,664
; REFERENCE/DOCKET NUMBER: 7WK-060548-00233
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 313-965-1976
; TELEFAX: 313-965-1951
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: N/A
; TOPOLOGY: N/A
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE: N/A
; ORGANISM: N/A
; PUBLICATION INFORMATION:
; AUTHORS: N/A
; TITLE: N/A
US-08-436-703B-4

Query Match 31.6%; Score 84; DB 2; Length 33;
Best Local Similarity 62.9%; Pred. No. 0.029;
Matches 22; Conservative 3; Mismatches 6; Indels 4; Gaps 1;

Qy 1 AKKAYAKKAYAKKAAKAAKAAKAAKAAK 35
| | | | | | | | | | | | | | | | | | | |
Db 3 AKKAAKAAKAAKAAKAAKAAKAAKAAK 33
| | | | | | | | | | | | | | | | | | | |

RESULT 15

US-08-152-488-12
; Sequence 12, Application US/08152488
; Patent No. 5534619
; GENERAL INFORMATION:
; APPLICANT: Wakefield, Thomas W.
; APPLICANT: Andrews, Philip C.
; APPLICANT: Stanley, James C.
; TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
; TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN

; TITLE OF INVENTION: ANTICOAGULATION REVERSAL
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Benita J. Rohm, Esq.
; STREET: 512 Springfield Avenue
; CITY: Cranford
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07016-1811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6; ASCII (DOS)Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/152,488
; FILING DATE: 12-NOV-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rohm, Benita J.
; REGISTRATION NUMBER: 28,664
; REFERENCE/DOCKET NUMBER: RM-7WG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-276-3344
; TELEFAX: 908-276-5543
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; STRANDEDNESS: N/A
; TOPOLOGY: N/A
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE: N/A
; ORGANISM: N/A
; PUBLICATION INFORMATION:
; AUTHORS: N/A
; TITLE: N/A
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
US-08-152-488-12

Query Match 29.9%; Score 79.5; DB 1; Length 29;
Best Local Similarity 69.0%; Pred. No. 0.07;
Matches 20; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

Qy 7 KEXAYAKKAAKAAKAAKAAKAAKAAK 35
| | | | | | | | | | | | | | | | | | | |
Db 2 KKKA-AKKA-AKKA-AKKA-AKKA-AKKA 29
| | | | | | | | | | | | | | | | | | | |

Search completed: June 3, 2005, 10:38:40
Job time : 43 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	79	25.2	62	2	T30977	hypothetical prote
2	68.5	21.9	45	2	S10544	protamine phi-3.2
3	68.5	21.9	45	2	S04941	protamine phi-3.1
4	68.5	21.9	45	2	S10545	protamine phi-3.3
5	60	19.2	58	2	A87439	hypothetical prote
6	56	17.9	45	4	A87435	antifreeze protein
7	55.5	17.7	44	2	P00028	tandem repeat pep
8	55	17.6	63	2	F83293	hypothetical prote
9	52.5	16.8	66	2	I6131	metallothionein ol
10	51.5	16.5	66	2	A86729	mercuric reductase
11	51	16.3	51	2	A56371	collagen alpha 1(X
12	50.5	16.1	62	2	H64443	hypothetical prote
13	50.5	16.1	65	2	A95330	hypothetical prote
14	50	16.0	40	1	PDI18G	antifreeze protein
15	49.5	15.8	64	2	S70831	ribosomal protein
16	49	15.7	56	2	T09177	ydae protein - Esc
17	49	15.7	61	2	A64163	ribosomal protein
18	49	15.7	62	2	H86286	hypothetical prote
19	48.5	15.5	34	2	B40186	ubiquitin / riboso
20	48.5	15.5	54	2	S78292	ribosomal protein
21	48.5	15.5	58	2	S78240	ribosomal protein
22	48.5	15.5	66	2	AD3327	hypothetical prote
23	48	15.3	55	2	S77143	hypothetical prote
24	48	15.3	58	2	T07317	ribosomal protein
25	48	15.3	59	2	S73128	ribosomal protein
26	48	15.3	60	2	S60851	M protein precursor
27	48	15.3	62	2	F69532	hypothetical prote
28	48	15.3	64	2	T13381	hypothetical prote
29	47.5	15.2	57	2	A83778	hypothetical prote

C; Superfamily: mercuroic resistance operon regulatory protein; heavy-metal-associated hox

Query Match 16.5%; Score 51.5; DB 2; Length 66;
Best Local Similarity 36.4%; Pred. No. 5.7e+02;
Matches 16; Conservative 3; Mismatches 16; Indels 9; Gaps 1;

OY 8 EKAYAKKAEAAKKAEEAKKYAKAEEKEEYAAEAEEKY 51
||| ||| ||| :: | :| ||| ||
DB 30 EKAQVSLKKNEALV-----KFSPADMDKMVAVAEAGYK 64

RESULT 11
AS6371 collagen alpha 1(XI) chain, alternative exon 2b - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 15-Sep-2003
C:Accession: A56371
R;Zhidkova, N.I.; Justice, S.K.; Wayne, R.
J. Biol. Chem. 270, 9486-9493, 1995
A:title: Alternative mRNA processing occurs in the variable region of the pro-alpha 1(XI)
A:Reference number: A56371; UID:95238468; PMID:7721876
A:Accession: A56371
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-51 <RES>
A:Cross-references: GB:L38956; NID:9840644; PIDN:AAA79171.1; PID:g1017460
C:Genetics:
A:Gene: GDB:COL1A1
A:Cross-references: GDB:L20595; OMIM:120280
A:Map position: lp21-lp21

Query Match 16.3%; Score 51; DB 2; Length 51;
Best Local Similarity 31.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 13; Mismatches 18; Indels 2; Gaps 1;

OY 2 KYVKEEKAYAKKAEAAKKAEEAKKYAKAEEKEEYAAEAEEK 49
||| ||| ||| :: | :| ||| ||
DB 2 KKSFNFKXOVRTATKSEKSKFTTPPKSEK--SSKKKKSYQAQAK 47

RESULT 12
H64443 hypothetical protein MJ1153 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: H64443
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
rson, J.D.; Sadov, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A:title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschi
A:Reference number: A64300; UID:96337999; PMID:8688087
A:Accession: H64443
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-62 <BU>
A:Cross-references: UNIPROT:Q58553; GB:U67557; GB:L77117; NID:g1591777; PIDN:AAB99159.1;
C:Genetics:
A:Map position: FOR1089904-1090092

Query Match 16.1%; Score 50.5; DB 2; Length 62;
Best Local Similarity 40.0%; Pred. No. 6.5e+02;
Matches 16; Conservative 6; Mismatches 13; Indels 5; Gaps 2;

OY 2 KKAYAK--KEKAYAKAK---KAEAKAEEKEEYAAEAEEKY 36
:|:|| |:| ||| ||| ||| |:| :|
DB 8 QKWAKMKGHYKYPKWLIAEQAEKMTLEBEKEWIEKA 47

RESULT 13
A95330 hypothetical protein SMA1009 [imported] - Sinorhizobium meliloti (strain 1021) magaplasma

Search completed: June 3, 2005, 10:57:34
Job time : 40 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2005, 10:38:45 ; Search time 172 Seconds
(without alignments)
196.496 Million cell updates/sec

Title: US-10-792-311-4

Perfect score: 313

Sequence: 1 AKYAKKAYAKAKAEK.....EAKYKAEAKAAKAEAYEA 66

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 115592

Minimum DB seq length: 0

Maximum DB seq length: 66

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82.5	26.4	60	Q9U3W3	Q9u3w3 caenorhabdi
2	82	26.2	66	Q95Q20	Q95q20 caenorhabdi
3	79.5	25.4	61	Q9NFJ7	Q9nfj7 trypanosoma
4	79	25.2	62	Q17536	Q17536 caenorhabdi
5	78	24.9	61	Q9NFJ5	Q9nfj5 trypanosoma
6	77.5	24.8	66	Q9NEJ3	Q9nej3 trypanosoma
7	76	24.3	66	Q9N578	Q9n578 rhodospseudo
8	73	23.3	35	Q747M3	Q747m3 geobacter s
9	72	23.0	42	Q9DF18	Q9df18 myoxocephal
10	70.5	22.5	57	Q82PG4	Q82pg4 streptomyce
11	68.5	21.9	43	Q6MGW9	Q6mgw9 bdellovibri
12	68.5	21.9	45	PH13 MYTCA	P11860 mytilus cal
13	67	21.4	44	Q7IIF2	Q7iif2 lactobacill
14	66.5	21.2	64	Q83AG7	Q83ag7 coxiella bu
15	62.5	20.0	62	Q9C2J3	Q9c2j3 neurospora
16	62.5	20.0	63	Q653G8	Q653g8 oryza sativ
17	61.5	19.6	53	MAR3 LEIMA	P14700 leishmania
18	61.5	19.6	66	Q73FW2	Q73fw2 wolbachia p
19	60.5	19.3	62	Q89G28	Q89g28 bradyrhizob
20	60.5	19.3	66	Q9FN38	Q9fn38 arabidopsis
21	60	19.2	58	Q9A834	Q9a834 caulobacter
22	59.5	19.0	63	Y9D1 RHIME	Q92xv9 rhizobium m
23	59.5	19.0	65	Q6FL16	Q6fl16 candida gla
24	59	18.8	61	Q7SLJ3	Q7slj3 neurospora
25	58.5	18.7	57	Y8A88_STRAW	Q82p45 streptomyce
26	58	18.5	54	Q97314	Q97314 plasmodium
27	58	18.5	55	Q8N6F0	Q8n6f0 homo sapien
28	58	18.5	57	Y678 STRCO	Q9rj87 streptomyce
29	57	18.2	42	Q96RT9	Q96rt9 homo sapien
30	57	18.2	62	Q75AP5	Q75ap5 ashbya goss
31	56.5	18.1	66	YH23_STRP3	Q7cen9 streptococc

32	56.5	18.1	66	1	YK05_STRPY	Q99xv5 streptococc
33	56.5	18.1	66	2	Q7CMQ8	Q7cmq8 streptococc
34	56	17.9	45	1	ANP8_MYOSC	P04368 myoxocephal
35	56	17.9	58	1	Y738_STRAW	Q82py3 streptomyce
36	55.5	17.7	66	1	Y600_STRAS	Q8e6g8 streptococc
37	55.5	17.7	66	1	Y619_STRAS	Q8e0v1 streptococc
38	55	17.6	63	2	Q9I035	Q9i035 pseudomonas
39	54.5	17.4	50	2	Q711P1	Q711p1 lactobacill
40	54	17.3	37	2	Q74CW2	Q74cw2 geobacter s
41	54	17.3	59	2	Q86965	Q86965 maize dwarf
42	54	17.3	62	2	Q8JKJ3	Q8jkj3 heliothis z
43	54	17.3	66	2	Q9FFA4	Q9ffa4 arabidopsis
44	53.5	17.1	51	2	Q7RF81	Q7rf81 plasmodium
45	53.5	17.1	66	1	Y606_STRAS	Q8e0w1 streptococc

ALIGNMENTS

RESULT 1
Q9U3W3 PRELIMINARY; PRT; 60 AA.
AC Q9U3W3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Histone H1.Q (Histone h1 like protein 7, isoform c).
GN Name=hil-7; ORFNames=C01B10.5;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Jedrusik M.A., Schulze E.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=Bristol N2;
RC MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN=Bristol N2;
RC Blanchard M., Bradshaw H.;
RT "The sequence of C. elegans cosmid C01B10.";
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA STRAIN=Bristol N2;
RC Waterston R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA STRAIN=Bristol N2;
RC Wilson R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA STRAIN=Bristol N2;
RC Wilson R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RA STRAIN=Bristol N2;
RC WormBase Consortium;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF216291; AAF23175.1; -;
DR EMBL; U58757; AAK66021.1; -;
DR WormBase; WBGene00001858; hil-7.


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Query Match      26.2%; Score 82; DB 2; Length 66;
Best Local Similarity 42.6%; Pred. No. 11;
Matches 26; Conservative 7; Mismatches 22; Indels 6; Gaps 2;

QY      6 KKEKAVAKAEEAAKAAKAAKAAKAYAKAAAEKKYEAAAEEAK---YKAEEAAKAAAKEA 62
DB      5 QKAKVAKYTKV---AAKPAPVKPKYFLKIQAAPKAAAPKAAKPPVKVKAANKSPAKKA 61

QY      63 A 63
DB      |-----|
        62 A 62

RESULT 3
Q9NFJ7 PRELIMINARY; PRT; 61 AA.
ID ID Q9NFJ7
AC AC Q9NFJ7
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Histone H1.
GN Name=H1A61;
OS Trypanosoma brucei gambiense.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=31285; [1]
RN SEQUENCE FROM N.A.
RP RC STRAIN=STIB 755;
RA Grueter B.;
RL Thesis (2000), Department of Parasitology, Institute of Zoology, SWITZERLAND. [2]
RC SEQUENCE FROM N.A.
RP RC STRAIN=STIB 755;
RA Grueter B., Betschart B.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
DR ENBL; AJ287597; CAB76179.1; -
SQ SEQUENCE 61 AA; 6059 MW; F600CB6D6D6DA73F CRC64;

Query Match      25.4%; Score 79.5; DB 2; Length 61;
Best Local Similarity 49.2%; Pred. No. 16;
Matches 29; Conservative 1; Mismatches 24; Indels 5; Gaps 2;

QY      9 KAYAKAKGAEEAAKAAKAAKAAKAYAKA---AK--AEKYEAAAEEAKYKAAEAKEAAKEA 62
DB      3 KAAGAPKCAVAKAAPPKCAVAKVAATKPLAKKVAGKKVVAKKYAPKVVAGKKAACKA 61

RESULT 4
Q17536 PRELIMINARY; PRT; 62 AA.
ID ID Q17536
AC AC Q17536;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Histone h1 like protein 7, isoform a.
GN Names=hil-7; ORFNames=C01B10.5;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nemata; Chromadorea; Rhabdita; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239; [1]
RN SEQUENCE FROM N.A.
RP RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018 (1998). [2]
RN SEQUENCE FROM N.A.
RP RC STRAIN=Bristol N2;
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QV 1 AKCYAKCKEYAKAKKAEAKAKKAEAKKAKAEKKEYAAAAEKYAEAAKAAK 60

[illegible]

[illegible]

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2005, 10:37:59 ; Search time 158.Seconds
(without alignments)
161.558 Million cell updates/sec

Title: US-10-792-311-4

Perfect score: 313

Sequence: 1 AKYAKKEKAYAKKAEAK.....EAKYAEAAKAAKAAEAAEAA 66

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1029624

Minimum DB seq length: 0

Maximum DB seq length: 66

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04.*

1: geneseqp1980s.*

2: geneseqp1990s.*

3: geneseqp2000s.*

4: geneseqp2001s.*

5: geneseqp2002s.*

6: geneseqp2003as.*

7: geneseqp2003bs.*

8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	313	100.0	66	3 AAY82574	Aay82574 Copolymer
2	198	63.3	56	3 AAY82573	Aay82573 Copolymer
3	120.5	38.5	45	3 AAY82572	Aay82572 Copolymer
4	105.5	33.7	35	3 AAY82571	Aay82571 Copolymer
5	103.5	33.1	56	8 ADO43176	Ado43176 Peptide u
6	102	32.6	46	2 AAW24449	Aaw24449 Nucleic a
7	98	31.3	60	5 AAG71043	Aag71043 Tumour ne
8	97.5	31.2	49	8 ADO43172	Ado43172 Peptide u
9	94	30.0	46	2 AAR28871	Aar28871 High affi
10	89.5	28.6	60	8 ADO04487	Ado04487 Sea urchi
11	89.5	28.6	60	8 ADS15345	Adsl5345 Yeast zuo
12	84	26.8	61	2 AAW08392	Aaw08392 Nucleic a
13	84	26.8	61	2 AAW38225	Aaw38225 Peptide u
14	84	26.8	61	2 AAW69201	Aaw69201 Nucleic a
15	84	26.8	61	2 AAW52872	Aaw52872 Nucleic a
16	84	26.8	66	5 AAE13239	Aae13239 Human lin
17	83.5	26.7	55	5 AAE13240	Aae13240 Human lin
18	83.5	26.7	61	8 ADO04488	Ado04488 Chicken h
19	83.5	26.7	61	8 ADS15346	Adsl5346 Yeast zuo
20	82	26.2	32	2 AAR90180	Aar90180 Polycatio
21	82	26.2	32	2 AAW06686	Aaw06686 Protamine
22	82	26.2	33	2 AAR90181	Aar90181 Polycatio
23	82	26.2	33	2 AAW06688	Aaw06688 Protamine
24	81.5	26.0	55	2 AAY34069	Aay34069 Histone H
25	81.5	26.0	55	2 AAY57367	Aay57367 Human his

26	81	25.9	56	8 ADO43179	Ado43179 Peptide u
27	81	25.9	65	6 ABU21642	Abu21642 Protein e
28	79.5	25.4	37	2 AAW08401	Aaw08401 Nucleic a
29	79.5	25.4	37	2 AAW69205	Aaw69205 Nucleic a
30	79.5	25.4	55	3 AAG40992	Aag40992 Zea maye
31	79	25.2	40	3 AAB08170	Aab08170 Peptide m
32	78	24.9	59	7 ADE10601	Adel10601 Structura
33	78	24.9	59	8 ADK15620	Adk15620 Nucleatin
34	77.5	24.8	66	3 AAG40982	Aag40982 Zea maye
35	77	24.6	45	2 AAW24450	Aaw24450 Nucleic a
36	77	24.6	45	3 AAY98493	Aay98493 Peptide #
37	77	24.6	45	3 AAY59038	Aay59038 Peptide u
38	77	24.6	45	4 AAB45846	Aab45846 Nucleic a
39	77	24.6	45	4 AAU04283	Aau04283 Trimeric
40	77	24.6	53	4 AAU18248	Aau18248 Novel hum
41	77	24.6	53	5 AEG92669	Age92669 Human DNA
42	77	24.6	53	7 ADC25386	Adc25386 Human ext
43	77	24.6	59	3 AAY98495	Aay98495 Nucleic l
44	77	24.6	59	3 AAY59040	Aay59040 Nucleic l
45	77	24.6	59	4 AAB45848	Aab45848 Nucleic a

ALIGNMENTS

RESULT 1

AAY82574

ID AAY82574 standard; peptide; 66 AA.

XX AC AAY82574;

XX DT 28-JUL-2000 (first entry)

XX DE Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:4.

XX KW Copolymer; molecular weight marker; TV-marker; immune disease;
 KW glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective;
 KW osteopathic; immunosuppressive; antichyroid; antiinflammatory;
 KW antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological;
 KW antianaemic; immunosuppressive; demyelinating disease; osteoarthritis;
 KW inflammatory condition; multiple sclerosis; rheumatoid arthritis;
 KW Crohn's disease; chronic immune thrombocytopaenia purpura; colitis;
 KW diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis;
 KW Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
 KW pemphigus vulgaris; systemic lupus erythematosus.

XX OS Unidentified.

XX PN WO200018794-A1.

XX PD 06-APR-2000.

XX PF 24-SEP-1999; 99WO-US022402.

XX PR 25-SEP-1998; 98US-0101693P.

XX PA (YEDA) YEDA RES & DEV CO LTD.

XX PI (TEVA-) TEVA PHARM USA INC.

XX PI Gad A, Lis D;

XX DR WPI; 2000-317499/27.

XX PT Copolymer 1 related polypeptides used as molecular weight markers for
 PT glatiramer acetate and for treatment and prevention of immune diseases.

XX PS Claim 10; Page 14; 72pp; English.

XX CC AAY82571 to AAY82577 represent specifically claimed copolymer molecular
 CC weight TV-marker polypeptides from the present invention. The present
 CC invention describes polypeptides (I) for determining the molecular weight
 CC of a copolymer (CP), which has an identified molecular weight and an
 CC amino acid composition corresponding to the copolymer. The polypeptides

AA Copolymer 1 related polypeptides used as molecular weight markers for PT glatiramer acetate and for treatment and prevention of immune diseases. PT

CC	For example, nano-tag elements can be attached to a peptide that has
CC	active groups (in the present case, lysine) at specific appropriately
CC	spaced sites. The peptide is then exposed to a mono-functionalised nano-
CC	tag element and all of the active sites are modified. The methods allow
CC	the sequencing of long nucleic acid sequences in a single sequencing run,
CC	high speed of obtaining sequence data, low cost of sequencing and high
CC	efficiency in terms of operator time, and sensitive and accurate
CC	detection and/or identification of nucleic acids with low incidence of
XX	false positive results.
XX	
SQ	Sequence 49 AA;
	Query Match 31.2%; Score 97.5; DB 8; Length 49;
	Best Local Similarity 58.5%; Pred. No. 0.011;
	Matches 31; Conservative 0; Mismatches 17; Indels 5; Gaps 1
QY	10 AYAKAKKAEAKAKAKAEAKCKAKAKAEKKYAAAEAKYKAEEAKAAKEA 62
DB	
	1 AAAAAKAAAAYKAAAAKAAAAKAAAAKA-----AAAAKAAAAKAAAAA 48
RESULT 9	
AAR28871	ID ID AAR28871 standard; peptide; 46 AA.
XX	AC AC AAR28871;
XX	
DT	23-MAR-2003 (revised)
DT	25-MAR-1993 (first entry)
XX	
DE	High affinity macrophage mannose receptor ligand compound #9.
XX	
KW	glycopeptide; mannose; mannosylated; glycosylated; mannose receptor;
KW	macrophages; monocytes; destroy; cytotoxicity; label; image; alter;
KW	macrophage processing of antigen; MHC restriction; inflammation;
KW	inflammatory diseases; macrophage secretory products; Crohn's disease;
KW	legionnaires disease; mononuclear phagocytes; HIV; AIDS;
KW	lysosomal storage diseases; Gaucher's disease; asthma;
KW	alveolar macrophages metastasis; systemic macrophages; deliver;
KW	antigenic peptides; prevent transplant rejection; organ transplantation;
KW	antitumour agents; cancer; toxins.
OS	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	Modified-site 1
FT	/note= "opt may have mannose, fucose, glucose or N-Ac-
FT	glucosamine. May also have non interfering subsits."
FT	Modified-site 4
FT	/note= "opt may have mannose, fucose, glucose or N-Ac-
FT	glucosamine."
FT	Modified-site 7
FT	/note= "opt may have mannose, fucose, glucose or N-Ac-
FT	glucosamine."
FT	Modified-site 10
FT	/note= "opt may have mannose, fucose, glucose or N-Ac-
FT	glucosamine."
FT	Modified-site 13
FT	/note= "opt may have mannose, fucose, glucose or N-Ac-
FT	glucosamine."
FT	Modified-site 16
FT	/note= "opt may have mannose, fucose, glucose or N-Ac-
FT	glucosamine."
FT	Modified-site 19
FT	/note= "opt may have mannose, fucose, glucose or N-Ac-
FT	glucosamine."
FT	Modified-site 22
FT	/note= "opt may have mannose, fucose, glucose or N-Ac-
FT	glucosamine."
FT	Modified-site 25
FT	/note= "opt may have mannose, fucose, glucose or N-Ac-
FT	glucosamine."
FT	Modified-site 28
FT	/note= "opt may have mannose, fucose, glucose or N-Ac-
FT	glucosamine."

FT /note= "opt may have mannose, fucose, glucose or N-Ac-
 FT glucosamine."
 FT 31
 FT Modified-site
 FT /note= "opt may have mannose, fucose, glucose or N-Ac-
 FT glucosamine."
 FT 34
 FT Modified-site
 FT /note= "opt may have mannose, fucose, glucose or N-Ac-
 FT glucosamine."
 FT 37
 FT Modified-site
 FT /note= "opt may have mannose, fucose, glucose or N-Ac-
 FT glucosamine."
 FT 40
 FT Modified-site
 FT /note= "opt may have mannose, fucose, glucose or N-Ac-
 FT glucosamine."
 FT 43
 FT Modified-site
 FT /note= "opt may have mannose, fucose, glucose or N-Ac-
 FT glucosamine."
 FT 46
 FT Modified-site
 FT /note= "opt may have mannose, fucose, glucose or N-Ac-
 FT glucosamine. May also have non interfering subunits."
 FT
 PN WO9219248-A1.
 XX
 XX 12-NOV-1992.
 PD
 XX
 XX 01-MAY-1992; 92WO-US003609.
 PF
 XX
 XX 03-MAY-1991; 91US-00694983.
 PR
 XX
 XX (UNIW) UNIV WASHINGTON.
 PA
 XX
 XX Stahl PD;
 PI
 PI
 XX
 XX WPI; 1992-398516/48.
 DR
 XX
 XX New high affinity mannose receptor ligand cpds. - for treating diseases
 FT mediated by macrophage activity e.g. asthma, inflammatory diseases and
 FT infectious diseases, e.g. HIV.
 PT
 XX
 XX Claim 3; Page 21; 32pp; English.
 PS
 XX
 CC This compound represents a glycopeptide effective in inhibiting the
 CC binding of labelled mannose BSA to mannose receptors. Mannose
 CC receptors are uniquely found on macrophages and not on monocytes.
 CC Glycopeptides such as this provide a mechanism to target macrophages
 CC specifically, to image, label, destroy or otherwise alter their antigen
 CC processing function. In addition they can be conjugated to solid supports
 CC and used to purify mannose receptors from a variety of sources. They are
 CC useful in the treatment of inflammatory diseases driven by macrophage
 CC secretory products eg. Crohn's disease; infectious diseases in which
 CC macrophages harbour replicating infectious agents eg. Legionnaires
 CC disease; viral infections involving mononuclear phagocytes eg. HIV and
 CC lysosomal storage diseases, in which macrophages are principally involved
 CC eg. Gaucher's disease; aschma mediated by alveolar macrophages; and in
 CC controlling metastasis, mediated by systemic macrophages. The peptides
 CC can also be used to deliver antigenic peptides as conjugates to a
 CC macrophage to marshal an immune response; also self peptides to prevent
 CC tissue transplant rejection. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 XX Sequence 46 AA;

Query Match 30.0%; Score 94; DB 2; Length 46;
 Best Local Similarity 64.6%; Pred. No. 0.022;
 Matches 31; Conservative 3; Mismatches 8; Indels 6; Gaps 3;
 QY 12 AKAKKAEAKAKAKAK-ABAKKYAKAKAEKKEKYAAAEAKYKAEAKAA 58
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 3 AKAKA-AKAKAKAKAKAKAKAKAKAKAK-AAA-AAA-AAA-AAA-AAA 45
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 10
 ADO04487

ID ADO04487 standard; protein; 60 AA.
 XX
 AC ADO04487;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Sea urchin histone H1 variant protein.
 XX
 XX Macroscopic membrane; cell growth; EAK16; Z-DNA binding protein; zuotin;
 KW medical product; suture; artificial skin; internal lining;
 KW slow-diffusion drug delivery system; protein-type drug; erythropoietin;
 KW haemoglobin; insulin; cell adhesion; cell migration; Alzheimer's disease;
 KW scrapie infection; sea urchin; histone; H1; variant.
 XX
 OS Arbacia punctulata.
 XX
 XX US2004087013-A1.
 PN
 XX 06-MAY-2004.
 PD
 XX
 XX 17-MAR-2003; 2003US-00390472.
 PF
 XX
 XX 28-DEC-1992; 92US-00973326.
 PR
 XX 22-AUG-1994; 94US-00293284.
 PR
 XX 26-MAR-1997; 97US-00824515.
 PR
 XX (HOLM/) HOLMES T.
 PA (ZHAN/) ZHANG S.
 PA (RICH/) RICH A.
 PA (DIPE/) DIPERSIO C M.
 PA (LOCK/) LOCKSHIN C.
 XX
 XX Holmes T, Zhang S, Rich A, Dipersio CM, Lockshin C;
 PI
 PI WPI; 2004-356208/33.
 DR
 XX
 PT Novel EAK16 protein incorporated into macroscopic membranes, useful in
 PT biomaterial applications such as medical products, artificial skin or
 PT internal linings, slow-diffusion drug delivery systems for in vitro cell
 PT growth.
 PT
 XX
 XX Example 5; SEQ ID NO 16; 56pp; English.
 PS
 CC The invention relates to a method for in vitro cell culture which
 CC involves adding a macroscopic membrane that is formed by self-assembly of
 CC amphiphilic peptide in an aqueous solution containing monovalent metal
 CC cations to a cell culture medium comprising cells, thus forming a
 CC membrane/culture mixture, maintaining the mixture under conditions
 CC sufficient for cell growth. The invention also relates to EAK16 peptide
 CC derived from yeast Z-DNA binding protein (zuotin). Zuotin incorporated
 CC into the macroscopic membranes are useful in biomaterial applications
 CC such as medical products (e.g., sutures), artificial skin or internal
 CC linings, slow-diffusion drug delivery systems supports for in vitro cell
 CC growth or culture and support for artificial tissue for in vivo use, as
 CC slow-diffusion drug delivery vehicle for delivering protein-type drugs
 CC e.g., erythropoietin, synthetic haemoglobin, insulin, etc., useful as
 CC conductive biopolymer for culturing cell monolayers, for promoting cell
 CC adhesion and migration, useful as experimental models for Alzheimer's
 CC disease and scrapie infection. The present sequence is sea urchin histone
 CC H1 variant protein. This sequence is used to illustrate the method of the
 CC invention.
 XX
 XX Sequence 60 AA;

Query Match 28.6%; Score 89.5; DB 8; Length 60;
 Best Local Similarity 56.8%; Pred. No. 0.081;
 Matches 25; Conservative 2; Mismatches 14; Indels 3; Gaps 1;

QY 2 KKYAKKEKAYAKKA---EAKAKKAKAEAKKYAKAKAEKKE 42
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 14 KAAAKKAAAKAKAKAKKPKKAAKAKKAKKPKKAKKPKKAKK 57
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||


```

RESULT 11
ADSL5345
ID ADSL5345 standard; protein; 60 AA.
XX
AC
XX ADSL5345;
XX
DT
XX
DE 16-DEC-2004 (first entry)
XX
DE Yeast zootin homologue sea urchin H1 delta.
XX
KW cell culture; macroscopic membrane; amphiphilic peptide; biomaterial;
KW slow-diffusion drug delivery system; artificial skin; separation matrix;
KW Alzheimer's disease; scrapie; liver cirrhosis; kidney amyloidosis;
KW protein conformational disease; yeast; DNA binding protein; zootin;
KW sea urchin; H1 delta.
XX
OS Paracentrotus lividus.
XX
XX
XX PN US6800481-B1.
XX
XX PD 05-OCT-2004.
XX
XX PF 26-MAR-1997; 97US-00824513.
XX
XX PR 28-DEC-1992; 97US-009733326.
XX
XX PR 22-AUG-1994; 94US-00293284.
XX
XX PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX
XX PI Holmes T, Zhang S, Rich A, Dipersio CM, Lockshin C;
XX
XX DR WPI; 2004-707224/69.
XX
XX
XX PT Culturing cells, in vitro, by adding macroscopic membrane formed by self-
XX assembly of amphiphilic peptides and monovalent metal cations, to form
XX PT culture mixture, and maintaining culture mixture under conditions for
XX PT cell growth.
XX
XX PS Example 5; SEQ ID NO 16; 50pp; English.
XX
XX CC The invention describes a method of culturing (M1) cells, in vitro. The
XX cell culture involves adding a macroscopic membrane which is formed by
XX self-assembly of amphiphilic peptides in an aqueous solution containing
XX monovalent metal cations, where the peptides have alternating hydrophobic
XX and hydrophilic amino acids and are complementary and structurally
XX compatible, to a cell culture medium comprising cells, thus forming a
XX membrane/culture mixture, and maintaining the mixture under conditions
XX sufficient for cell growth. (M1) is useful for culturing a macroscopic
XX membrane utilised in biomaterial applications e.g., slow-diffusion drug
XX delivery systems, artificial skin or separation matrices, or as
XX experimental models for Alzheimer's disease and scrapie infection e.g.,
XX liver cirrhosis, kidney amyloidosis, or other protein conformational
XX diseases. (M1) enables in vitro culturing of macroscopic membrane that is
XX stable in aqueous solution, serum and ethanol, highly resistant to heat,
XX alkaline and acidic pH, chemical denaturants and proteolytic digestion,
XX and is non-cytotoxic. This is the amino acid sequence of a region found
XX in sea urchin histone H1 delta which is homologous to yeast DNA binding
XX protein zootin from which amphiphilic peptides capable of forming
XX membrane can be isolated.
XX
XX SQ Sequence 60 AA;
XX
XX Query Match 28.6%; Score 89.5; DB 8; Length 60;
XX Best Local Similarity 56.8%; Pred. No. 0.081;
XX Matches 25; Conservative 2; Mismatches 14; Indels 3; Gaps 1;
XX
XX QY 2 KKYAKKEAYAKKA---EAKAKKAKAEAKKAKAKAEKKE 42
XX | | | | | | | | | | | | | | | | | | | |
XX 14 KAAAKKAAKAAKAKKPKKAAKAKKAKKPKKAKKPKKAKK 57
XX
XX RESULT 12
AAW08392

```


XX 16-AUG-1996; 96GB-00017214.
 PR 28-AUG-1996; 96US-0025040P.
 XX
 PA (MEDI-) MEDICAL RES COUNCIL.
 XX
 PI Antoniou M, Grosveld PG;
 XX
 DR WPI, 1998-169179/15.
 XX
 XX Self-replicating, episomal vector for tissue-restricted expression of
 PT genes - includes origin of replication and locus control region.
 PT optionally used with second vector expressing replication protein.
 XX
 PS Disclosure; Page 33; 66pp; English.
 XX
 CC This sequence represents a nucleic acid condensing peptide, that can be
 CC used to deliver the vector of the invention. The vector is a self-
 CC replicating, episomal DNA expression vector (A) for expressing a gene (I)
 CC comprises: (a) a self-replicating origin of replication (ori) and (b) a
 CC locus control region (LCR), or its component, that when linked to (I)
 CC directs expression of (I) in a tissue-restricted manner. (A) and the
 CC vector pair are used for tissue-restricted expression of (I) in cultured
 CC cells; in vivo, particularly for gene therapy, e.g. of cancer, or ex
 CC vivo, for subsequent return of transduced cells. Transgenic animals are
 CC used to test fidelity and efficacy of tissue-restricted expression before
 CC clinical trials, also for long-term production of (I)-encoded proteins.
 CC (A) provide stable gene expression over at least 10-15 cell generations
 XX
 SQ Sequence 61 AA;

Query Match 26.8%; Score 84; DB 2; Length 61;
 Best Local Similarity 45.8%; Pred. NO. 0.29;
 Matches 27; Conservative 8; Mismatches 22; Indels 2; Gaps 2;

Qy 2 KKYAKCKKAYAKAKAEAKAKAEAKKYAKAKAEK-KEYAAAEAKYKAEAKAA 59
 || :|: ||| ||: ||||: | ||||: | | :| |
 Db 3 KKRKVKKSPKKAKPAKSPAKAKAVK-PKAAPKKPKKKRVEKSPKAKKPAA 60

Search completed: June 3, 2005, 10:52:53
 Job time : 159 secs

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Search completed: June 3, 2005, 11:09:50
Job time : 139 secs

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	313	100.0	66	4	US-09-405-743A-4	Sequence 4, Appli
2	313	100.0	66	4	US-09-816-989A-4	Sequence 4, Appli
3	198	63.3	56	4	US-09-405-743A-3	Sequence 3, Appli
4	198	63.3	56	4	US-09-816-989A-3	Sequence 3, Appli
5	120.5	38.5	45	4	US-09-405-743A-2	Sequence 2, Appli
6	120.5	38.5	45	4	US-09-816-989A-2	Sequence 2, Appli
7	117.5	37.5	56	3	US-08-993-008A-6	Sequence 6, Appli
8	107	34.2	48	3	US-08-993-008A-5	Sequence 5, Appli
9	105.5	33.7	35	4	US-09-405-743A-1	Sequence 1, Appli
10	105.5	33.7	35	4	US-09-816-989A-1	Sequence 1, Appli
11	89.5	28.6	60	1	US-08-346-849-16	Sequence 16, Appl
12	89.5	28.6	60	2	US-08-293-284A-16	Sequence 16, Appl
13	89.5	28.6	60	4	US-08-898-300-16	Sequence 16, Appl
14	89.5	28.6	60	4	US-08-824-513-16	Sequence 16, Appl
15	84	26.8	61	3	US-08-995-172-6	Sequence 6, Appli
16	84	26.8	61	3	US-08-995-172-7	Sequence 7, Appli
17	84	26.8	61	4	US-09-221-050-7	Sequence 7, Appli
18	84	26.8	61	4	US-09-247-054-11	Sequence 11, Appl
19	83.5	26.7	61	1	US-08-346-849-17	Sequence 17, Appl
20	83.5	26.7	61	2	US-08-293-284A-17	Sequence 17, Appl
21	83.5	26.7	61	4	US-08-898-300-17	Sequence 17, Appl
22	83.5	26.7	61	4	US-08-824-513-17	Sequence 17, Appl
23	82.5	26.4	61	4	US-09-247-054-15	Sequence 15, Appl
24	82	26.2	32	1	US-08-152-488-13	Sequence 13, Appl
25	82	26.2	32	1	US-08-303-025-15	Sequence 15, Appl
26	82	26.2	32	2	US-08-677-304-13	Sequence 13, Appl
27	82	26.2	32	2	US-08-436-703B-2	Sequence 2, Appli

US-09-816-989A-3

Query Match	63.3%	Score 198;	DB 4;	Length 56;
Best Local Similarity	80.3%;	Pred. No.	1.1e-12;	
Matches	53:	Conservative	2:	Mismatches
				Indels
				Gaps

[illegible]

Qy 61 EAAVEA 66
|||
pb 51 EAAVEA 56

RESULT 5

US-09-405-743A-2
; Sequence 2, Application US/09405743A

; Patent No. 6514938

APPLICANT: Yeda Research and Development Co., Ltd.

TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS

FILE REFERENCE: 60807-A

;; CURRENT APPLICATION NUMBER: US/09/405,743A
: CURRENT FILING DATE: 1999-09-24

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 2
: L. LENGTH: 41
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; LENGTH: 13
; TYPE: PRT

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; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER TN:
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OTHER INFORMATION: DESCRIPTION OF ALLICINAT SEQUENCE:
; OTHER INFORMATION: PEPTIDE

US-09-405-743A-2

Q: How many matches did you play?

Query Match	36.3%;	Score 120.3; DB 4; Length 43;
Best Local Similarity	71.1%;	Pred. No. 2.5e-05;
Matches	32.	Conservative
Matches	0.	Mismatches
Matches	6.	Indels
Matches	7.	Gaps

Qy 29 AKKYAKAAKAE--KKEYAAAEK-----YKAEAAKAAKAAAYEA 66

Dp 1 AKKYAKKAAEKAKKAYKAAFAKAAKYKAAAEKAAKAAKAAAYEA 45

RESULT 6
IIS-09-816-999X-2

RESULT 4

GENERAL INFORMATION:
 ; APPLICANT: Gad, Alexander
 : APPLICANT: Lis. Doris

TITLE OF INVENTION

; TITLE OF INVENTION:

FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816.989A

; CURRENT FILING DATE: 2001-03-23

; PRIOR APPLICATION NUMBER: 60/

; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22402

PRIOR FILING DATE: 1999-09-24

; NUMBER OF SEQ ID NOS: 7

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2

```

```

; SEQ ID NO 2
;
; LENGTH: 45

```



```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-2

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Query Match 38.5%; Score 120.5; DB 4; Length 45;
Best Local Similarity .71.1%; Pred. No. 2.5e-05;
Matches 32; Conservative 0; Mismatches 6; Indels 7; Gaps 2;

Qy 29 AKKYAKAAKAE--KKEYAAAEAK-----YKAEAAKAAKAEAAEYEA 66
||||| ||||| ||| ||||| ||| ||||| |||||
Db 1 AKKYAKKAAEKAKKAYKAAEAKKAAKYEKAAAEKAAKAEAAEYEA 45

RESULT 7
US-08-993-008A-6
; Sequence 6, Application US/08993008A
; Patent No. 6153596

PATENT NO. 6135396
 GENERAL INFORMATION:
 APPLICANT: Liotta, Dennis C.
 APPLICANT: Petros, John A.
 APPLICANT: Wey, Shiow-Jyi
 APPLICANT: Karr, Joan F.
 APPLICANT: Pohl, Jan
 TITLE OF INVENTION: Polycationic Oligomers
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Greenlee, Winner and Sullivan
 STREET: 5370 Manhattan Circle, Suite 201
 CITY: Boulder
 STATE: CO
 COUNTRY: US

```

? ZIP: 80303
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent In Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/993,008A
?
```

:
 : FILING DATE: 18-DEC-1997
 :
 : CLASSIFICATION: 514
 :
 : PRIOR APPLICATION DATA:
 :
 : APPLICATION NUMBER: US 60/032,436
 :
 : FILING DATE: 18-DEC-1996
 :
 : ATTORNEY/AGENT INFORMATION:
 :
 : NAME: Sullivan, Sally A.
 :
 : REGISTRATION NUMBER: 32,064
 :
 : REFERENCE/DOCKET NUMBER: 33-95
 :
 : TELECOMMUNICATION INFORMATION:
 :
 : TELEPHONE: 303-499-8080
 :
 :

TELEFAX: 303-499-8089 6:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 56 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-931-0082-6

Query Match	37.5%	Score 117.5;	DB 3;	Length 56;
Best Local Similarity	65.5%	Pred. No. 6e-05;		
Matches	36:	Conservative	5:	Mismatches 11:
				Indels 3:
				Gaps 3:

[illegible]

db

```

RESULT 8
US-08-993-008A-5
Sequence 5, Application US/08993008A
Patent No. 6153596
GENERAL INFORMATION:
APPLICANT: Liotta, Dennis C.
APPLICANT: Petros, John A.
APPLICANT: Wey, Shioan-Jyi
APPLICANT: Karr, Joan F.
APPLICANT: Pohl, Jan
TITLE OF INVENTION: Polycationic Oligomers
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESS: Greenlee, winner and Sullivan
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993, 008A
FILING DATE: 18-DEC-1997

CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US 60/032,436
FILING DATE: 18-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sullivan, Sally A.
REGISTRATION NUMBER: 32,064
REFERENCE/DOCKET NUMBER: 33-95
TELECOMMUNICATION INFORMATION:

TELEPHONE: 303-499-8080
TELEFAX: 303-499-8089
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-993-008A-5

Query Match 34.2%; Score 107; DB 3; Length 48;
Best Local Similarity 64.6%; Pred. No. 0.00053;
Matches 31: Conservative 5; Mismatches 10; Indels

QY	9	KAYAKAK - KAEFAKAAKKAKAEAKKYAKA - AKAEKKEYAAEAERKYAKAEA	54
		: : :	
Dd	1	KA	48

RESULT 9
US-09-405-743A-1
; Sequence 1, Application US/09405743A
; Patent No. 6514938
; GENERAL INFORMATION:

```

: GENERAL INFORMATION:
: APPLICANT: Yeda Research and Development Co., Ltd.
: TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
: FILE REFERENCE: 60807-A
: CURRENT APPLICATION NUMBER: US/09/405,743A
: CURRENT FILING DATE: 1999-09-24
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: PatentIn ver. 2.1
: SEQ ID NO 1
: LENGTH: 35
: TYPE: PRT

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PEPTIDE
US-09-405-743A-1

Query Match          33.7%; Score 105.5; DB 4; Length 35;
Best Local Similarity 43.9%; Pred. No. 0.00053;
Matches 29; Conservative 2; Mismatches 4; Indels 31; Gaps 1;

Qy 1 AKKYAKKEKAYAKAKAEAKKAAKAEAKKYAKAEKKEYYAAAEAKKYAEAAKAAK 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 AKKYAKKEKAAKAYKKEA-----KAKAEAAK 29

Qy 61 EAAYEA 66
    |||||
Db 30 EAAYEA 35

RESULT 10
US-09-816-989A-1
; Sequence 1, Application US/09816989A
; Patent No. 6800287
; GENERAL INFORMATION:
; APPLICANT: Gad, Alexander
; APPLICANT: Lie, Doris
; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
; TITLE OF INVENTION: AND FOR THERAPEUTIC USE
; FILE REFERENCE: 2609/60807-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/816,989A
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/101,693
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22402
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-1

Query Match          33.7%; Score 105.5; DB 4; Length 35;
Best Local Similarity 43.9%; Pred. No. 0.00053;
Matches 29; Conservative 2; Mismatches 4; Indels 31; Gaps 1;

Qy 1 AKKYAKKEKAYAKAKAEAKKAAKAEAKKYAKAEKKEYYAAAEAKKYAEAAKAAK 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 AKKYAKKEKAAKAYKKEA-----KAKAEAAK 29

Qy 61 EAAYEA 66
    |||||
Db 30 EAAYEA 35

RESULT 11
US-08-346-849-16
; Sequence 16, Application US/08346849
; Patent No. 5670483
; GENERAL INFORMATION:
; APPLICANT: Zhang, Shuguang
; APPLICANT: Lockshin, Curtis
; APPLICANT: Rich, Alexander
; APPLICANT: Holmes, Todd
; TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
; TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,284A
; FILING DATE: 22-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 07/973,326
```

```
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346,849
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,326
; FILING DATE: 28 DECEMBER 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: MIT-6008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-346-849-16

Query Match          28.6%; Score 89.5; DB 1; Length 60;
Best Local Similarity 56.8%; Pred. No. 0.032;
Matches 25; Conservative 2; Mismatches 14; Indels 3; Gaps 1;

Qy 2 KKYAKKEKAYAKAKA---EAKAAKKAAKAAKAYAKAAKAAKKE 42
    | | | | | | | | | | | | | | | | | | | | | | | |
Db 14 KAAAKKAAKAAKAAKAKKPKKAAKAAKAAKAAKPKKAAKPKK 57

RESULT 12
US-08-293-284A-16
; Sequence 16, Application US/08293284A
; Patent No. 5955343
; GENERAL INFORMATION:
; APPLICANT: Holmes, Todd
; APPLICANT: Zhang, Shuguang
; APPLICANT: Rich, Alexander
; APPLICANT: DiPersio, C. Michael
; APPLICANT: Lockshin, Curtis
; TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
; TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,284A
; FILING DATE: 22-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 07/973,326
```


; FILING DATE: 28-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: MIT-6008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-293-284A-16

Query Match 28.6%; Score 89.5; DB 2; Length 60;
Best Local Similarity 56.8%; Pred. No. 0.032;
Matches 25; Conservative 2; Mismatches 14; Indels 3; Gaps 1;

Qy 2 KKYAKKEKAYAKAKA---EAKAAKKAABAKKYAKAAKAEKKE 42
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 14 KAAAKRKAATAAKAKKPKKKAATAAKKAKKPKKPKKAKKPAKK 57

RESULT 13
US-08-898-300-16
; Sequence 16, Application US/08898300
; Patent No. 6548630
; GENERAL INFORMATION:
; APPLICANT: Zhang, Shuguang
; APPLICANT: Lockshin, Curtis
; APPLICANT: Rich, Alexander
; APPLICANT: Holmes, Todd
; TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
; TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 22 JULY 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,849
; FILING DATE: 30 NOVEMBER 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,326
; FILING DATE: 28 DECEMBER 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: MIT-6008FB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-898-300-16

Query Match 28.6%; Score 89.5; DB 4; Length 60;
Best Local Similarity 56.8%; Pred. No. 0.032;
Matches 25; Conservative 2; Mismatches 14; Indels 3; Gaps 1;

Qy 2 KKYAKKEKAYAKAKA---EAKAAKKAABAKKYAKAAKAEKKE 42
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 14 KAAAKRKAATAAKAKKPKKKAATAAKKAKKPKKPKKAKKPAKK 57

RESULT 14
US-08-824-513-16
; Sequence 16, Application US/08824513
; Patent No. 6800481
; GENERAL INFORMATION:
; APPLICANT: Holmes, Todd
; APPLICANT: Zhang, Shuguang
; APPLICANT: Rich, Alexander
; APPLICANT: DiPersio, C. Michael
; APPLICANT: Lockshin, Curtis
; TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
; TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: March 26, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/293,284
; FILING DATE: August 22, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,326
; FILING DATE: 28 DECEMBER 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: MIT-6008A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-824-513-16

Query Match 28.6%; Score 89.5; DB 4; Length 60;
Best Local Similarity 56.8%; Pred. No. 0.032;
Matches 25; Conservative 2; Mismatches 14; Indels 3; Gaps 1;

Qy 2 KKYAKKEKAYAKAKA---EAKAAKKAABAKKYAKAAKAEKKE 42
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 14 KAAAKRKAATAAKAKKPKKKAATAAKKAKKPKKPKKAKKPAKK 57

RESULT 15
US-08-995-172-6


```
; Sequence 6, Application US/08995172B
; Patent No. 6218112
; GENERAL INFORMATION:
; APPLICANT: Thatcher, David R
; APPLICANT: Wilks, Paula E
; TITLE OF INVENTION: Optimization of Gene Delivery and Gene Delivery Systems
; FILE REFERENCE: CAC00026
; CURRENT APPLICATION NUMBER: US/08/995,172B
; CURRENT FILING DATE: 1997-12-22
; EARLIER APPLICATION NUMBER: 60/033,908
; EARLIER FILING DATE: 1996-12-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-08-995-172-6

Query Match      26.8%; Score 84; DB 3; Length 61;
Best Local Similarity 45.8%; Pred. No. 0.11; 22; Indels 2; Gaps 2;
Matches 27; Conservative 8; Mismatches 22; Indels 2; Gaps 2;

Qy      2 KKYAKKEKAYAKAKAEAKAKAEAKKYAKAKAEK-KEYAAAAEAKYKAEAAAA 59
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      3 KKRKVEKSPKAKKPAKSPAKAKAVK-PKAAKPKPKKKRVEKSPKAKKPA 60
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
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Search completed: June 3, 2005, 10:58:21
Job time : 43 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	82	22.4	62	2	T30977	hypothetical prote
2	76	20.8	45	2	S04941	protamine phi-3.1
3	73	19.9	45	2	S10545	protamine phi-3.3
4	72	19.7	45	2	S10544	protamine phi-3.2
5	71	19.4	69	1	NSTR6	nonhistone chromos
6	64.5	17.6	71	2	G83572	30S ribosomal prot
7	63	17.2	73	2	A02579	histone H1.4 - rab
8	60	16.4	58	2	S58143	gene 14 protein -
9	60	16.4	70	2	S07510	gene 4.3 protein -
10	59.5	16.3	74	2	G69966	hypothetical prote
11	59	16.1	68	2	S78710	protein YDL085c-a
12	58	15.8	58	2	A87439	hypothetical prote
13	58	15.8	72	2	S58762	ribosomal protein
14	58	15.8	72	2	S58760	ribosomal protein
15	57.5	15.7	54	2	S78292	ribosomal protein
16	57.5	15.7	58	2	S78240	ribosomal protein
17	57	15.6	56	2	T07842	probable histone H
18	57	15.6	64	2	S61536	myosin heavy chain
19	57	15.6	64	2	T22415	hypothetical prote
20	55.5	15.2	64	2	S70831	ribosomal protein
21	55	15.0	45	2	A05163	antifreeze protein
22	55	15.0	65	2	A95330	hypothetical prote
23	55	15.0	67	2	A64321	archaeal histone -
24	55	15.0	67	2	D64416	archaeal histone -
25	54.5	14.9	60	2	S60851	M protein precurs
26	54	14.8	51	2	A56371	collagen alpha 1(X
27	54	14.8	67	2	T146866	alpha-myosin heavy
28	54	14.8	67	2	T14467	pollen coat protei
29	54	14.8	68	2	G69093	histone HMTA2 - Me

QY 1 AKKYAKKEKAYAKAEAKKAAEAKAYAKAEAKKAAEAKKAAEAKKYAK 45
||: :||: || :||: || :||: || :||: ||
Db 3 AKRSRKKKAHVKK---SSKSKAKKPKSPKKKKAACKPAKKAACK 43

RESULT 3

S10545
protamine phi-3.3 - California mussel
N;Alternate names: protamine PL-IV.3
C;Species: Mytilus californianus (California mussel)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: S10545
R;Ausio, J.; McParland, R.
Eur. J. Biochem. 182, 569-576, 1989
A;Title: Sequence and characterization of the sperm-specific protein phi3 from Mytilus
A;Reference number: S04941; MUID:89325302; PMID:2666130
A;Accession: S10545
A;Molecule type: protein
A;Residues: 1-45 <AUS>
A;Cross-references: UNIPROT:P11860
C;Superfamily: histone H1
C;Keywords: DNA binding; nucleus

Query Match 19.9%; Score 73; DB 2; Length 45;
Best Local Similarity 42.2%; Pred. No. 18;
Matches 19; Conservative 9; Mismatches 13; Indels 4; Gaps 1;

QY 1 AKKYAKKEKAYAKAEAKKAAEAKAYAKAEAKKAAEAKKAAEAKKYAK 45
||: :||: || :||: || :||: || :||: ||
Db 3 AKRSRKKKAHVKK---SSKSKAKKPKSPKKKKAACKPAKKAACK 43

RESULT 4

S10544
protamine phi-3.2 - California mussel
N;Alternate names: protamine PL-IV.2
C;Species: Mytilus californianus (California mussel)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: S10544
R;Ausio, J.; McParland, R.
Eur. J. Biochem. 182, 569-576, 1989
A;Title: Sequence and characterization of the sperm-specific protein phi3 from Mytilus
A;Reference number: S04941; MUID:89325302; PMID:2666130
A;Accession: S10544
A;Molecule type: protein
A;Residues: 1-45 <AUS>
A;Cross-references: UNIPROT:P11860
C;Superfamily: histone H1
C;Keywords: DNA binding; nucleus

Query Match 19.7%; Score 72; DB 2; Length 45;
Best Local Similarity 42.2%; Pred. No. 21;
Matches 19; Conservative 8; Mismatches 14; Indels 4; Gaps 1;

QY 1 AKKYAKKEKAYAKAEAKKAAEAKAYAKAEAKKAAEAKKAAEAKKYAK 45
||: :||: || :||: || :||: || :||: ||
Db 3 AKRSRKKKAHVKK---SSKSKAKKPKSPKKKKAACKPAKKAACK 43

RESULT 5

NSTR6
nonhistone chromosomal protein H6 - rainbow trout
N;Alternate names: histone I
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 30-Sep-1979 #sequence_revision 08-Oct-1981 #text_change 09-Jul-2004
C;Accession: A02653
R;Watson, D.C.; Wong, N.C.W.; Dixon, G.H.
Eur. J. Biochem. 95, 193-202, 1979
A;Title: The complete amino-acid sequence of a trout-testis non-histone protein, H6, loc
A;Reference number: A02653; MUID:79213375; PMID:456349
A;Accession: A02653
A;Molecule type: protein

A;Residues: 1-69 <WAT>
A;Cross-references: UNIPROT:P02315
A;Experimental source: testis
A;Note: This protein was formerly called histone T
C;Superfamily: nonhistone chromosomal protein HMG-17
C;Keywords: chromosomal protein, DNA binding, nucleus

Query Match 19.4%; Score 71; DB 1; Length 69;
Best Local Similarity 36.9%; Pred. No. 35;
Matches 24; Conservative 5; Mismatches 36; Indels 0; Gaps 0;

QY 13 KKAEEAKKAAKAYKAEAKKKAKAEAKKYAKAAEAKKEKYAAAAEKYKAEAAKAAKE 72
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 4 KSATKGDEPARRSARLSARPVPKPAAPKPKAAAPKAVGKGAENGDAKAEAKVQAAGD 63
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY 73 AAYEA 77
DB 64 GAGNA 68

RESULT 6
G83572
30S ribosomal protein S21 PA0579 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
R;Accession: G83572
C;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bcs
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathoge
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: G83572
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-71 <STO>
A;Cross-references: UNIPROT:Q915V8; GB:AE004494; GB:AE004091; NID:g9946446; PIDN:AAG03966
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: rpsU; PA0579
C;Superfamily: Escherichia coli ribosomal protein S21

Query Match 17.6%; Score 64.5; DB 2; Length 71;
Best Local Similarity 30.6%; Pred. No. 1.1e+02;
Matches 15; Conservative 12; Mismatches 17; Indels 5; Gaps 1;

QY 9 KAYAKKAEKAAKAEAKYK-----AAEAKKAKAEAKKYAKAAAEKK 52
::: ||| :::: ||| : ||| : ||| : ||| : ||| :
DB 17 RRFKRCEKAGVLAEVRSEFYEPKTAERKKRAAAAARKHAKKVQREQR 65

RESULT 7
A02579
histone H1.4 - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C;Accession: A02579
R;Hall, S.C.; Cole, R.D.
J. Biol. Chem. 246, 7175-7190, 1971
A;Title: Amino acid sequence and sequence variability of the amino-terminal regions of ly
A;Reference number: A02578; MUID:72068710; PMID:5167020
A;Accession: A02579
A;Molecule type: protein
A;Residues: 1-73 <RAL>
A;Cross-references: UNIPROT:P02252
R;Langan, T.A.; Hall, S.C.; Cole, R.D.
J. Biol. Chem. 246, 1942-1944, 1971
A;Reference number: A37504; MUID:71134818; PMID:5547708
A;Contents: annotation
C;Superfamily: histone H1
C;Keywords: acetylated amino end; chromosomal protein; DNA binding; nucleosome; nucleus;
F;1/Modified site: acetylated amino end (Ser) #status experimental
F;37/Binding site: phosphate (Ser) (covalent) #status experimental


```

Query Match      17.2%; Score 63; DB 2; Length 75;
Best Local Similarity 32.3%; Pred. No. 1.4e+02;
Matches 21; Conservative 11; Mismatches 33; Indels 0; Gaps 0;

QY   9 KAVAKAEKAAKKAAYKAAAEKKAKAEEAKKYAKAAEKKYAKAAEKKYAAAEEAKYKAAEA 68
DB   2 EAPAEVTAAPAKSPATPVVKARKKKSAGNAEKKGPPVSELIITXAVAASKERSGVSLA 61

QY   69 AAKEA 73
DB   62 ALKKA 66

RESULT 8
S58143
gene 14 protein - phage SPPI
C:Species: phage SPPI
C>Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C:Accession: S58143; T42284
R;Becker, B.; Gassel, M.; Tavares, P.; Lurz, R.; Alonso, J.C.
submitted to the EMBL Data Library, July 1995
A:Description: Head morphogenesis of the Bacillus subtilis bacteriophage SPPI.
A:Reference number: S58137
A:Accession: S58143
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-58 <BEC>
A:Cross-references: UNIPROT:Q38583; EMBL:X89721; NID:g1052805; PIDN:CAA61871.1; PID:g1052805
R;Alonso, J.C.; Luder, G.; Stiege, A.C.; Chai, S.; Weise, F.; Trautner, T.A.
Gene 204, 201-212, 1997
A:Title: The complete nucleotide sequence and functional organization of Bacillus subtilis bacteriophage SPPI.
A:Reference number: Z22137; MUID:98094274; PMID:9434185
A:Accession: T42284
A>Status: preliminary; translated from GB/EMBL/DDBB
A:Molecule type: DNA
A:Residues: 1-58 <ALO>
A:Cross-references: EMBL:X97918; PIDN:CAA66545.1

Query Match      16.4%; Score 60; DB 2; Length 58;
Best Local Similarity 39.6%; Pred. No. 1.9e+02;
Matches 19; Conservative 7; Mismatches 20; Indels 2; Gaps 2;

QY   1 AKKYAKKEKAYAKKAEEAKKAAKAAKAAKAAEKKKAAEKKKAAEAKKYAKAAK 48
DB   11 AKQREKERBAARKAER-EKKASEKQKGAQ-KPKDKSECKSTRKPPK 56

RESULT 9
S07510
gene 4.3 protein - phage T3
C:Species: phage T3
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: S07510
R;Beck, P.J.; Gonzalez, S.; Ward, C.L.; Molineux, I.J.
J. Mol. Biol. 210, 687-701, 1989
A:Title: Sequence of bacteriophage T3 DNA from gene 2.5 through gene 9.
A:Reference number: S07500; MUID:90133923; PMID:2614843
A:Accession: S07510
A:Molecule type: DNA
A:Residues: 1-70 <BEC>
A:Cross-references: UNIPROT:P20317; EMBL:X17255; NID:g15682; PIDN:CAA35138.1; PID:g15682
C:Genetics:
A:Gene: 4.3
C:Superfamily: phage T7 gene 4.3 protein

Query Match      16.4%; Score 60; DB 2; Length 70;
Best Local Similarity 35.4%; Pred. No. 2.2e+02;
Matches 17; Conservative 9; Mismatches 22; Indels 0; Gaps 0;

QY   1 AKKYAKKEKAYAKKAEEAKKAAKAAEKKKAAEKKKAAEAKKYAKAAK 48
DB   20 AKKLDDKADSORAIELAKOSRKSDPAAYSGVHKSAIAIAKAOQSMK 67

```


C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: A87439
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
N.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of *Caulobacter crescentus*.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: A87439
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-58 <STO>
A;Cross-references: UNIPROT:Q9A834; GB:AE005673; NID:gl3422913; PIDN:AAK23509.1; GSPDB:G
C;Genetics:
A;Gene: CCI530

Query Match 15.8%; Score 58; DB 2; Length 58;
Best Local Similarity 36.8%; Pred. No. 2.7e+02;
Matches 14; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 14 KAEEAKKAKAEAKYKAAEAKKAEAKYKAAEAKKAEAK 51
DB 9 QAKAKAKADKKARATENVRFGRSKAEKSLERAEAK 46

RESULT 13
S58762
ribosomal protein S20 - Klebsiella pneumoniae (fragment)
C;Species: Klebsiella pneumoniae
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S58762; S71843
R;Nemec, A.; Haywood-Farmer, A.; Mackie, G.A.
Biochim. Biophys. Acta 1263, 154-158, 1995
A;Title: Conserved amino acid residues in the primary structure of ribosomal protein S20
A;Reference number: S58760; MUID:95367591; PMID:7640306
A;Accession: S58762
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-72 <NEW>
A;Cross-references: UNIPROT:P45601; EMBL:U20493
submitted to the EMBL Data Library, January 1995
A;Reference number: S71843
A;Accession: S71843
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-63, 'R', 65-72 <MAC>
A;Cross-references: EMBL:U20493; NID:g665953; PIDN:AAA86999.1; PID:g665954
C;Superfamily: Escherichia coli ribosomal protein S20
C;Keywords: protein biosynthesis; ribosome

Query Match 15.8%; Score 58; DB 2; Length 72;
Best Local Similarity 39.0%; Pred. No. 3.2e+02;
Matches 16; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 28 KAEEAKKAKAEAKYKAAEAKKAEAKYKAAEAKKAEAK 68
DB 2 RAVQSEKARKHNASRRSMRTFFIKVYAAIEAGDKAAQAQA 42

RESULT 14
S58760
ribosomal protein S20 - Salmonella typhimurium (fragment)
C;Species: Salmonella typhimurium
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 09-Jul-2004
C;Accession: S58760
R;Nemec, A.; Haywood-Farmer, A.; Mackie, G.A.
Biochim. Biophys. Acta 1263, 154-158, 1995
A;Title: Conserved amino acid residues in the primary structure of ribosomal protein S20
A;Reference number: S58760; MUID:95367591; PMID:7640306
A;Accession: S58760
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-72 <NEW>

A;Cross-references: UNIPROT:P41787; EMBL:U20491; NID:g665949; PIDN:AAA87001.1; PID:g66595;
C;Superfamily: Escherichia coli ribosomal protein S20
C;Keywords: protein biosynthesis; ribosome; RNA binding
Query Match 15.8%; Score 58; DB 2; Length 72;
Best Local Similarity 39.0%; Pred. No. 3.2e+02;
Matches 16; Conservative 6; Mismatches 19; Indels 0; Gaps 0;
QY 28 KAEEAKKAKAEAKYKAAEAKKAEAKYKAAEAKKAEAK 68
DB 2 RAVQSEKARKHNASRRSMRTFFIKVYAAIEAGDKAAQAQA 42

RESULT 15

S78292
ribosomal protein L32', chloroplast - Odontella sinensis chloroplast
C;Species: chloroplast Odontella sinensis
C;Date: 17-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 20-Jun-2000
C;Accession: S78292
R;Kowalik, K.V.; Stoebe, B.; Schaffran, I.; Kroth-Pancic, P.; Freier, U.
Plant Mol. Biol. Rep. 13, 336-342, 1995
A;Title: The Chloroplast Genome of a Chlorophyll a+c- containing Alga, *Odontella sinensis*
A;Reference number: S78238
A;Accession: S78292
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-54 <KOW>
A;Cross-references: EMBL:Z67753; NID:gl185127; PIDN:CAA91665.1; PID:gl185182
C;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995
C;Genetics:
A;Gene: rpl32'
A;Genome: chloroplast
C;Superfamily: rice chloroplast ribosomal protein L32
C;Keywords: chloroplast; protein biosynthesis; ribosome

Query Match 15.7%; Score 57.5; DB 2; Length 54;
Best Local Similarity 45.5%; Pred. No. 2.8e+02;
Matches 15; Conservative 6; Mismatches 11; Indels 1; Gaps 1;

QY 1 AKKYAKKEKAYAKKAEAKKAEAKKAEAKKAEAK 33
DB 11 AKKNARK-SVWKKKADKAKKKSLSLAKSVLQGG 42

Search completed: June 3, 2005, 11:16:14
Job time : 39 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	114	31.1	68	2	Q26907	trypanosoma
2	102.5	28.0	71	2	Q9NFJ8	trypanosoma
3	102	27.9	76	2	Q9N6J8	trypanosoma
4	102	27.3	76	2	Q9NFJ4	trypanosoma
5	100.5	27.5	71	2	Q9N6K5	trypanosoma
6	99	27.0	76	2	Q9NFF2	trypanosoma
7	99	27.0	76	2	Q9NFJ6	trypanosoma
8	96.5	26.4	71	2	Q9N6K0	trypanosoma
9	96	26.2	76	2	Q9N6N7	trypanosoma
10	96	26.2	76	2	Q9NFF1	trypanosoma
11	95	26.0	76	2	Q9N6I0	trypanosoma
12	92.5	25.3	75	2	Q9NFK0	trypanosoma
13	88	24.0	74	1	H1C8_TRYCR	trypanosoma
14	86	23.5	66	2	Q9NRFJ3	trypanosoma
15	85	23.2	60	2	Q9U3W3	caenorhabdi
16	82.5	22.5	61	2	Q9NFPJ5	trypanosoma
17	82.5	22.5	61	2	Q9NFPJ7	trypanosoma
18	82	22.4	62	2	Q17536	caenorhabdi
19	79	21.6	66	2	Q95Q20	caenorhabdi
20	78.5	21.4	44	2	Q71IY2	lactobacill
21	77.5	21.2	68	2	Q7RI34	plasmodium
22	76.5	20.9	43	2	Q6MGW9	bdellovibri
23	76	20.8	45	1	PHI3_MYTCA	mytilus cal
24	76	20.8	61	2	Q7SIJ3	neurospora
25	72.5	19.8	73	2	Q6MK36	bdellovibri
26	71	19.4	66	2	Q6N578	rhodopsedu
27	71	19.4	69	1	H6_ONCMY	oncorhynch
28	68	18.6	35	2	Q747M3	geobacter s
29	68	18.6	62	2	Q9C2J3	neurospora
30	67.5	18.4	66	2	Q9FN38	arabidopsis
31	67.5	18.4	67	2	Q8XW13	raletsonia s

	Query Match	27.5%	Score 100.5	DB 2	Length 71
	Best Local Similarity	50.0%	Pred. No. 1.4		
	Matches 38	Conservative 4	Mismatches 25	Indels 9	Gaps 4
Qy	1	AKKYAKKEKAYAKKA--EKAA--KKA	AKAYAAEAKKKA	EAKKYAKAAKAEKKEVAAA	57
Db	2	AKA	AAAPKAVAKAAAPKAAAPKAAVAK--KAA	PKAVAKAAAPKAAVAKAAAPKAVAK	59
Qy	58	EAKYKAEAAKAAAKEA	73		


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Db      60 ----KVAGKKAAYAKA 71

RESULT 6
Q9NFF2 ID Q9NFF2 PRELIMINARY; PRT; 76 AA.
AC Q9NFF2; 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Histone H1.
GN Name=H1B76;
OS Trypanosoma brucei brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TREU 927/4;
RA Grueter E.; Betschart B.;
RL Thesis (2000), Department of Parasitology, Institute of Zoology,
RL SWITZERLAND.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=TREU 927/4;
RA Grueter E.; Betschart B.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ400880; CAB90836.1; -.
SQ SEQUENCE 76 AA; 7631 MW; 2493E88448B3E0FD CRC64;

Query Match 27.0%; Score 99; DB 2; Length 76;
Best Local Similarity 50.6%; Pred. No. 1.9; Mismatches 3; Indels 6; Gaps 4;
Matches 39; Conservative 3;

Qy      1 AKKYAKKEKAYAKA--EKAA-KKAAKAYKAAEAKKKAAYAKA--AEKKEYAA 56
Db      2 AKTTAAKKAAYAKA--EKAA-KKAAKAYKAAEAKKKAAYAKA--AEKKEYAA 59
Qy      57 AEAKYKAAEAKKAAKEA 73
Db      60 KVAPKAVAGKKAAYAKA 76

RESULT 7
Q9NFF6 ID Q9NFF6 PRELIMINARY; PRT; 76 AA.
AC Q9NFF6; 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Histone H1.
GN Name=H1B76;
OS Trypanosoma brucei brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TREU 927/4;
RA Grueter E.; Betschart B.;
RL Thesis (2000), Department of Parasitology, Institute of Zoology,
RL SWITZERLAND.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=TREU 927/4;
RA Grueter E.; Betschart B.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ287539; CAB76182.1; -.
SQ SEQUENCE 76 AA; 7587 MW; 2959EF4982E2E0F9 CRC64;

Query Match 27.0%; Score 99; DB 2; Length 76;
Best Local Similarity 50.6%; Pred. No. 1.9; Mismatches 3; Indels 6; Gaps 4;
Matches 39; Conservative 3;

Qy      1 AKKYAKKEKAYAKA--EKAA-KKAAKAYKAAEAKKKAAYAKA--AEKKEYAA 56

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Db      2 AKASAAPKKAAYAKA--EKAA-KKAAKAYKAAEAKKKAAYAKA--AEKKEYAA 59
Qy      57 AEAKYKAAEAKKAAKEA 73
Db      60 KVAPKAVAGKKAAYAKA 76

RESULT 8
Q9N6K0 ID Q9N6K0 PRELIMINARY; PRT; 71 AA.
AC Q9N6K0; 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Histone H1.
GN Name=H1E71; Synonyms=H1A71;
OS Trypanosoma brucei brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TREU 927/4;
RA Grueter E.; Betschart B.;
RL Thesis (2000), Department of Parasitology, Institute of Zoology,
RL SWITZERLAND.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=TREU 927/4;
RA Grueter E.; Betschart B.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ400881; CAB90839.1; -.
SQ SEQUENCE 71 AA; 7005 MW; 478C7B6994847C80 CRC64;

Query Match 26.4%; Score 96.5; DB 2; Length 71;
Best Local Similarity 48.7%; Pred. No. 2.8;
Matches 37; Conservative 4; Mismatches 26; Indels 9; Gaps 4;

Qy      1 AKKYAKKEKAYAKA--EKAA-KKAAKAYKAAEAKKKAAYAKA--AEKKEYAA 57
Db      2 AKASAAPKKAAYAKA--EKAA-KKAAKAYKAAEAKKKAAYAKA--AEKKEYAA 59
Qy      58 EAKYKAAEAKKAAKEA 73
Db      60 ----KVAGKKAAYAKA 71

RESULT 9
Q9N6N7 ID Q9N6N7 PRELIMINARY; PRT; 76 AA.
AC Q9N6N7; 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Histone H1.
GN Name=H1D76; Synonyms=H1A76, H1C76;
OS Trypanosoma brucei brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TREU 927/4;
RA Grueter E.; Betschart B.;
RL Thesis (2000), Department of Parasitology, Institute of Zoology,
RL SWITZERLAND.
RN [2]
RP SEQUENCE FROM N.A.

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RC STRAIN=TREU 927/4;
RA Grueter E., Betschart B.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ287600; CAB76184.1; -.
DR EMBL; AJ287599; CAB76183.1; -.
DR EMBL; AJ287598; CAB76181.1; -.
DR GO; GO:0000786; C:nucleosome; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006334; P:nucleosome assembly; IEA.
DR InterPro; IPR005819; Histone_H5.
DR PRINTS; PR00624; HISTONEH5.
SQ SEQUENCE 76 AA; 7556 MW; 2959F33D5D5B0F9 CRC64;

Query Match 26.2%; Score 96; DB 2; Length 76;
Best Local Similarity 49.4%; Pred. No. 3.2;
Matches 38; Conservative 5; Mismatches 28; Indels 6; Gaps 4;

QY 1 AKKYAKKEKAYAKKA--EKAA-KKAEAKYKAAAEAKKAKAEAKKYAKAKAEKKEYAAA 57
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 AKASAAPKKAVAKKAAAPKKAAPKKAVAK--KAAAPKKAVAKKAAAPKKAVAKKPLAKKAAAPK 59

QY 58 E-AKYKAEAAKAAKAA 73
   :|||:|||||:
Db 60 KVAPKKVAGKKAACKA 76

RESULT 10
Q9NFF1 ID Q9NFF1 PRELIMINARY; PRT; 76 AA.
AC Q9NFF1;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Histone H1.
GN Names=H176;
OS Trypanosoma brucei brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TREU 927/4;
RA Grueter E.;
RL Thesis (2000), Department of Parasitology, Institute of Zoology,
   SWITZERLAND.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=TREU 927/4;
RA Grueter E., Betschart B.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ287605; CAB76190.1; -.
DR EMBL; AJ287601; CAB76186.1; -.
SQ SEQUENCE 76 AA; 7573 MW; 6079EF4982B50767 CRC64;

Query Match 26.0%; Score 95; DB 2; Length 76;
Best Local Similarity 49.4%; Pred. No. 3.8;
Matches 38; Conservative 3; Mismatches 30; Indels 6; Gaps 4;

QY 1 AKKYAKKEKAYAKKA--EKAA-KKAEAKYKAAAEAKKAKAEAKKYAKAKA--AEKKEYAA 56
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 AKASAAPKKAVAKKAAAPKKAAPKKAVAK--KGAPKKAVAKKAAAPKKAVAKKPLAKKVVAK 59

QY 57 AEAKYKAEAAKAAKAA 73
   :|||:|||||:
Db 60 KVAPKKVAGKKAACKA 76

RESULT 12
Q9NFKO ID Q9NFKO PRELIMINARY; PRT; 75 AA.
AC Q9NFKO;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE Histone H1.
GN Names=H1A75;
OS Trypanosoma brucei gambiense.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=31285;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=STIB 755;
RA Grueter E.;
RL Thesis (2000), Department of Parasitology, Institute of Zoology,
   SWITZERLAND.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=STIB 755;
RA Grueter E., Betschart B.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ287592; CAB76174.1; -.
SQ SEQUENCE 75 AA; 7597 MW; 130AB85471996052 CRC64;

Query Match 25.3%; Score 92.5; DB 2; Length 75;
Best Local Similarity 51.4%; Pred. No. 5;
Matches 37; Conservative 1; Mismatches 25; Indels 9; Gaps 4;

QY 2 KKYAKKEKAYAKKAEAKYKAAAEAKKAKAEAKKYAKAKAEKKEYAAAEAKY 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 13 KKVAAK-KAVAKKA--APKKA--KAAAPKKAVAKKAAAPKKAVA----KKVAKKVVAPK 63
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RC STRAIN=TREU 927/4;
RA Grueter E., Betschart B.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ287600; CAB76184.1; -.
DR EMBL; AJ287599; CAB76183.1; -.
DR EMBL; AJ287598; CAB76181.1; -.
DR GO; GO:0000786; C:nucleosome; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006334; P:nucleosome assembly; IEA.
DR InterPro; IPR005819; Histone_H5.
DR PRINTS; PR00624; HISTONEH5.
SQ SEQUENCE 76 AA; 7556 MW; 2959F33D5D5B0F9 CRC64;

Query Match 26.2%; Score 96; DB 2; Length 76;
Best Local Similarity 49.4%; Pred. No. 3.2;
Matches 38; Conservative 5; Mismatches 28; Indels 6; Gaps 4;

QY 1 AKKYAKKEKAYAKKA--EKAA-KKAEAKYKAAAEAKKAKAEAKKYAKAKAEKKEYAAA 57
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 AKTAAPKKAVAKKAAAPKKAAPKKAVAK--KAAAPKKAVAKKAAAPKKAVAKKPLAKKAAAPK 59

QY 58 E-AKYKAEAAKAAKAA 73
   :|||:|||||:
Db 60 KVAPKKVAGKKAACKA 76

RESULT 11
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RP SEQUENCE FROM N.A.
RC STRAIN=427;
RA Grueter E., Betschart B.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ287608; CAB76193.1; -
SQ SEQUENCE 66 AA; 6593 MW; 2D664C3471064DC6 CRC64;

Query Match 23.5%; Score 86; DB 2; Length 66;
Best Local Similarity 48.0%; Pred. NO. 15;
Matches 36; Conservative 2; Mismatches 25; Indels 12; Gaps 4;

QY 1 AKKYAKKEKAYAKAEKAAKAEKAKVAKAEAKKKA--KAEAKKYAKAEKAEKKEYAAAE 58
DB ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 59 AKYKAEAAKAAKAAKEA 73
DB | | ||||| :
QY 52 APKKVAGKAAKAAKEA 66
DB | | ||||| :

RESULT 15
Q9U3W3 PRELIMINARY; PRT; 60 AA.
AC Q9U3W3;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 25-OCT-2004 (TEMBLrel. 28, Last annotation update)
DE Histone H1-Q (Histone h1 like protein 7, isoform c).
GN Name-hil-7; ORFNames=C01B10.5;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
[1]
RN RN
RP SEQUENCE FROM N.A.
RA Jedrusik M.A., Schulze E.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
[2]
RN RN
RP SEQUENCE FROM N.A.
RA STRAIN=Bristol N2;
RC MEDLINE=98069613; PubMed=9851916;
RX WormBase Consortium;
RG "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium. ";
RN Science 282:2012-2018 (1998).
[3]
RN RN
RP SEQUENCE FROM N.A.
RA STRAIN=Bristol N2;
RC Blanchard M., Bradshaw H.;
RL "The sequence of C. elegans cosmid C01B10." ;
RT Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
[4]
RN RN
RP SEQUENCE FROM N.A.
RA STRAIN=Bristol N2;
RC Waterston R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
[5]
RN RN
RP SEQUENCE FROM N.A.
RA STRAIN=Bristol N2;
RC Wilson R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
[6]
RN RN
RP SEQUENCE FROM N.A.
RA STRAIN=Bristol N2;
RC Wilson R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
[7]
RN RN
RP SEQUENCE FROM N.A.
RA STRAIN=Bristol N2;
RC WormBase Consortium;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF216291; AAF23175.1; -
DR EMBL; U59757; AAK66021.1; -

```


DR WormBase; WBGene00001858; h1l-7.
DR WormPep; CO1B10.5c; CE26857.
DR GO; GO:0000786; C:nucleosome; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006334; P:nucleosome assembly; IEA.
DR InterPro; IPR005819; Histone_H5.
DR PRINTS; PR00624; HISTONEH5.
SQ SEQUENCE 60 AA; 6212 MW; D01ABB4CEC35566D CRC64;

Query Match 23.2%; Score 85; DB 2; Length 60;
Best Local Similarity 43.4%; Pred. No. 16;
Matches 23; Conservative 4; Mismatches 26; Indels 0; Gaps 0;

Qy 1 AKKYAKKEKAYAKAEAKKAAKAYKAAEAKKKAAEAKKYAKKAAEAKKE 53
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 7 AKKVAKTKVAAKPKAPKPVKASPKKAAAPKAKKPVKAAAKKSPAKKAAPKK 59
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

Search completed: June 3, 2005, 11:15:30
Job time : 173 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2005, 10:57:41 ; Search time 157 Seconds
(without alignments)
189.685 Million cell updates/sec

Title: US-10-792-311-5
Perfect score: 366
Sequence: 1 AKYAKKAYAKAEKAAK.....EAKYKAEAKAAKEAYEA 77

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1079814

Minimum DB seq length: 0
Maximum DB seq length: 77

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	366	100.0	77	3 AAY82575	Aay82575 Copolymer
2	282.5	77.2	66	3 AAY82574	Aay82574 Copolymer
3	245.5	67.1	56	3 AAY82573	Aay82573 Copolymer
4	131	35.8	45	3 AAY82572	Aay82572 Copolymer
5	104.5	28.6	35	3 AAY82571	Aay82571 Copolymer
6	103.5	28.3	60	5 ABG71043	ABG71043 Tumour ne
7	101.5	27.7	46	2 AAW24449	Aaw24449 Nucleic a
8	101.5	27.7	56	8 ADO43176	Ado43176 Peptide u
9	101.5	27.7	60	8 ADO04487	Ado04487 Sea urchi
10	101.5	27.7	60	8 ADS15345	Adsl5345 Yeast zuo
11	99.5	27.2	46	2 AAR28871	Aar28871 High affi
12	98	26.8	75	7 ADE10646	Ade10646 Structura
13	98	26.8	75	8 ADK15665	Adk15665 Nucleatin
14	93	25.4	71	4 AAM17388	Aam17388 Peptide #
15	93	25.4	71	4 ABB36406	Abb36406 Peptide #
16	93	25.4	71	4 ABB21763	Abb21763 Protein #
17	93	25.4	71	4 AAM69569	Aam69569 Human bon
18	93	25.4	71	5 ABG39191	Abg39191 Human pep
19	92	25.1	61	2 AAW08392	Aaw08392 Nucleic a
20	92	25.1	61	2 AAW38225	Aaw38225 Peptide u
21	92	25.1	61	2 AAW69201	Aaw69201 Nucleic a
22	92	25.1	61	2 AAW52872	Aaw52872 Nucleic a
23	90	24.6	70	7 ADE10603	Ade10603 Structura
24	89	24.6	70	8 ADK15622	Adk15622 Nucleatin
25	89	24.3	61	8 ADO04488	Ado04488 Chicken h

26	89	24.3	61	8 ADS15346	Adsl5346 Yeast zuo
27	89	24.3	67	7 ADE10647	Ade10647 Structura
28	89	24.3	67	8 ADK15666	Adk15666 Nucleatin
29	89	24.3	69	8 ADR96126	Adr96126 Novel S.
30	89	24.3	75	4 AAO05530	Aao05530 Human pol
31	89	24.3	75	7 ADE10696	Ade10696 Structura
32	89	24.3	75	8 ADK15715	Adk15715 Library f
33	88.5	24.2	66	5 AAE13239	Aae13239 Human lin
34	88	24.0	49	8 ADO43172	Ado43172 Peptide u
35	87	23.8	70	7 ADE10653	Ade10653 Structura
36	87	23.8	70	8 ADK15672	Adk15672 Library f
37	86	23.5	59	3 AAY98495	Aay98495 Nucleat
38	86	23.5	59	3 AAY59040	Aay59040 Nucleat
39	86	23.5	59	4 AAB45848	Aab45848 Nucleic a
40	86	23.5	59	4 AAU04285	Aau04285 Nucleat
41	85	23.2	77	5 AAE13238	Aae13238 Human lin
42	84.5	23.1	32	2 AAR90180	Aar90180 Polycatio
43	84.5	23.1	32	2 AAW06686	Aaw06686 Protamine
44	84.5	23.1	33	2 AAR90181	Aar90181 Polycatio
45	84.5	23.1	33	2 AAW06688	Aaw06688 Protamine

ALIGNMENTS

RESULT 1
AAY82575
ID AAY82575 standard; peptide; 77 AA.

XX AC AAY82575;
XX
DT 28-JUL-2000 (first entry)
XX

DE Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:5.

XX
KW Copolymer; molecular weight marker; TV-marker; immune disease;
KW Glutramer acetate; autoimmune disease; antiarthritis; neuroprotective;
KW osteopathic; immunosuppressive; antithyroid; antipneumonia;
KW antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological;
KW antianemic; immunosuppressive; demyelinating disease; osteoarthritis;
KW inflammatory condition; multiple sclerosis; rheumatoid arthritis;
KW Crohn's disease; chronic immune thrombocytopenia purpura; colitis;
KW diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis;
KW Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
KW pemphigus vulgaris; systemic lupus erythematosus.

OS Unidentified.

XX WO200018794-A1.

XX 06-APR-2000.

XX 24-SEP-1999; 99WO-US022402.

XX 25-SEP-1998; 98US-0101693P.

XX (YEDA) YEDA RES & DEV CO LTD.
PA (TEVA-) TEVA PHARM USA INC.

XX Gad A, Lis D;

XX WPI; 2000-317499/27.

XX Copolymer 1 related polypeptides used as molecular weight markers for
glutramer acetate and for treatment and prevention of immune diseases.

XX Claim 10; Page 14; 72pp; English.

XX AAY82571 to AAY82577 represent specifically claimed copolymer molecular
weight TV-marker polypeptides from the present invention. The present
invention describes polypeptides (I) for determining the molecular weight
of a copolymer (CP), which has an identified molecular weight and an
amino acid composition corresponding to the copolymer. The polypeptides

CC of the invention are used as molecular weight markers for glatiramer
 CC acetate related tetrapolymers. The polypeptides may also be used for
 CC treating and preventing immune diseases in a mammal. Autoimmune diseases
 CC which may be treated include either cell-mediated or antibody-mediated
 CC diseases. Such diseases include arthritic conditions, demyelinating
 CC diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid
 CC arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune
 CC ophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, Crohn's
 CC disease, chronic immune thrombocytopaenia purpura, colitis, contact
 CC sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's
 CC syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis,
 CC psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-
 CC mediated diseases which can be treated include host-versus-graft disease,
 CC graft-versus-host disease, and delayed-type hypersensitivity. The
 CC polypeptides of the invention have defined molecular weights and physical
 CC properties which are analogous to glatiramer acetate molecules, which
 CC makes them ideal for use as molecular weight markers
 XX
 SQ Sequence 77 AA;

Query Match 100.0%; Score 366; DB 3; Length 77;
 Best Local Similarity 100.0%; Pred. No. 7.7e-27;
 Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKYAKKEKAYAKKAEKAKAEKAYKAAEAKKKAKAEKAYKAAKAEKKEKAYAAEAK 60
 DB 1 AKKYAKKEKAYAKKAEKAKAEKAYKAAEAKKKAKAEKAYKAAKAEKKEKAYAAEAK 60

QY 61 YKAEAAKAAKAEAAEAA 77
 DB 61 YKAEAAKAAKAEAAEAA 77

RESULT 2
 AAY82574
 ID AAY82574 standard; peptide; 66 AA.

XX AAY82574;
 AC AAY82574;
 DT 28-JUL-2000 (first entry)

DE Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:4.

XX Copolymer; molecular weight marker; TV-marker; immune disease;
 KW Glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective;
 KW osteopathic; immunosuppressive; antithyroid; antiinflammatory;
 KW antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological;
 KW antianaemic; immunosuppressive; demyelinating disease; osteoarthritis;
 KW inflammatory condition; multiple sclerosis; rheumatoid arthritis;
 KW Crohn's disease; chronic immune thrombocytopaenia purpura; colitis;
 KW diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis;
 KW Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
 KW pemphigus vulgaris; systemic lupus erythematosus.

XX Unidentified.

XX WO200018794-A1.

XX 06-APR-2000.

XX 24-SEP-1999; 99WO-US022402.

XX 25-SEP-1998; 98US-0101693P.

XX (YEDA) YEDA RES & DEV CO LTD.

XX (TEVA-) TEVA PHARM USA INC.

XX Gad A, Lis D;

XX WPI; 2000-317499/27.

XX Copolymer 1 related polypeptides used as molecular weight markers for
 PT glatiramer acetate and for treatment and prevention of immune diseases.

XX Claim 10; Page 14; 72pp; English.
 XX AAY82571 to AAY82577 represent specifically claimed copolymer molecular
 CC weight TV-marker polypeptides from the present invention. The present
 CC invention describes polypeptides (I) for determining the molecular weight
 CC of a copolymer (CP), which has an identified molecular weight and an
 CC amino acid composition corresponding to the copolymer. The polypeptides
 CC of the invention are used as molecular weight markers for glatiramer
 CC acetate related tetrapolymers. The polypeptides may also be used for
 CC treating and preventing immune diseases in a mammal. Autoimmune diseases
 CC which may be treated include either cell-mediated or antibody-mediated
 CC diseases. Such diseases include arthritic conditions, demyelinating
 CC diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid
 CC arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune
 CC ophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, Crohn's
 CC disease, chronic immune thrombocytopaenia purpura, colitis, contact
 CC sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's
 CC syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis,
 CC psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-
 CC mediated diseases which can be treated include host-versus-graft disease,
 CC graft-versus-host disease, and delayed-type hypersensitivity. The
 CC polypeptides of the invention have defined molecular weights and physical
 CC properties which are analogous to glatiramer acetate molecules, which
 CC makes them ideal for use as molecular weight markers
 XX
 SQ Sequence 66 AA;

Query Match 77.2%; Score 282.5; DB 3; Length 66;
 Best Local Similarity 84.4%; Pred. No. 3.6e-19;
 Matches 65; Conservative 0; Mismatches 1; Indels 11; Gaps 2;

QY 1 AKKYAKKEKAYAKKAEKAKAEKAYKAAEAKKKAKAEKAYKAAKAEKKEKAYAAEAK 60
 DB 1 AKKYAKKEKAYAKKAEKAKAEKAYKAAEAKKKAKAEKAYKAAKAEKKEKAYAAEAK 49

QY 61 YKAEAAKAAKAEAAEAA 77
 DB 50 YKAEAAKAAKAEAAEAA 66

RESULT 3
 AAY82573
 ID AAY82573 standard; peptide; 56 AA.

XX AAY82573;
 AC AAY82573;

XX 28-JUL-2000 (first entry)

DE Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:3.

XX Copolymer; molecular weight marker; TV-marker; immune disease;
 KW Glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective;
 KW osteopathic; immunosuppressive; antithyroid; antiinflammatory;
 KW antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological;
 KW antianaemic; immunosuppressive; demyelinating disease; osteoarthritis;
 KW inflammatory condition; multiple sclerosis; rheumatoid arthritis;
 KW Crohn's disease; chronic immune thrombocytopaenia purpura; colitis;
 KW diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis;
 KW Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
 KW pemphigus vulgaris; systemic lupus erythematosus.

XX Unidentified.

XX WO200018794-A1.

XX 06-APR-2000.

XX 24-SEP-1999; 99WO-US022402.

XX 25-SEP-1998; 98US-0101693P.

XX (YEDA) YEDA RES & DEV CO LTD.

AC AAW24449;
 XX
 DT 30-SEP-1997 (first entry)
 XX
 DE Nucleic acid (NA) binding peptide used in NA delivery to cells.
 XX
 DE Nucleic acid transporter; gene therapy; binding complex; lysis agent;
 KW JTS-1; K8; alpha helix; endosome; lysosome; nucleus targeting.
 XX
 OS Synthetic.
 XX
 XX WO9640958-A1.
 PN
 XX 19-DEC-1996.
 PD
 XX
 XX 23-APR-1996; 96WO-US005679.
 PF
 XX 07-JUN-1995; 95US-00484777.
 PR
 XX (BAYU) BAYLOR COLLEGE MEDICINE.
 PA
 XX Smith LC, Sparrow JT, Woo SL;
 PI
 XX WPI; 1997-052345/05.
 DR
 XX
 XX Nucleic acid transporter useful in gene therapy - contains binding
 PT complex associated with surface and nuclear ligands and lysis agent.
 PT
 XX Disclosure; Page 49; 125pp; English.
 PS
 XX
 XX AAW24434-W24459 are nucleic acid (NA) binding peptides, capable of both
 CC condensing and stabilising a NA. The peptides can be conjugated to a
 CC lytic peptide to form a nucleic acid transporter system. The lysis agent
 CC forms an alpha-helical structure. The transporter system is used to
 CC deliver nucleic acid to a cell and for treating humans by gene therapy.
 CC By taking advantage of the characteristics of both the lysis agents and
 CC the binding molecules, delivery of the nucleic acid is enhanced. Specific
 CC lysis agents are capable of releasing the nucleic acid into the cellular
 CC interior from the endosome. Release is efficient without
 CC endosomal/lysosomal degradation. Once released the binding complexes help
 CC target the nucleic acid to the nucleus
 XX
 SQ Sequence 46 AA;
 Query Match 27.7%; Score 101.5; DB 2; Length 46;
 Best Local Similarity 58.7%; Pred. No. 0.015;
 Matches 27; Conservative 6; Mismatches 12; Indels 1; Gaps 1;
 QY 17 KAKAKAEAKYKAEAKKAEAKKAEAKKAEAKKAEAKKAEAKKAEAKKAEAKK 62
 DB 2 KAKWK 46
 RESULT 8
 ADO43176
 ID ADO43176 standard; peptide; 56 AA.
 AC
 AC ADO43176;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Peptide used for coded probe synthesis.
 XX
 XX Nano-barcode; scanning probe microscopy; probe.
 KW
 OS Synthetic.
 XX
 XX WO2004038037-A2.
 PN
 XX 06-MAY-2004.
 PD
 XX
 XX 22-SEP-2003; 2003WO-US029726.
 PF
 XX

PR 20-SEP-2002; 2002US-00251152.
 PR 19-SEP-2003; 2003US-00667004.
 XX
 PA (ITLC) INTEL CORP.
 PI
 XX Chan S, Su X, Yamakawa M;
 XX
 DR WPI; 2004-399960/37.
 XX
 XX Detecting, identifying and sequencing of biomolecules using controlled
 PT alignment of nano-barcodes encoding specific information for scanning
 PT probe microscopy, useful in the fields of molecular biology.
 XX
 XX Example 2; Page 44; 63pp; English.
 XX
 CC The present sequence is that of a peptide of potential use for production
 CC of a coded probe useful in the method of the invention. The invention
 CC provides methods, apparatus and compositions for the detection,
 CC identification and/or sequencing of biomolecules, such as nucleic acids
 CC or proteins. Coded probes comprising a probe molecule attached to one or
 CC more nano-barcodes are allowed to bind to target molecule(s). After
 CC binding and separation from unbound coded probes, the bound coded probes
 CC are aligned on a surface and analysed by scanning probe microscopy (SPM).
 CC The methods allow the sequencing of long nucleic acid sequences in a
 CC single sequencing run, high speed of obtaining sequence data, low cost of
 CC sequencing and high efficiency in terms of operator time, and sensitive
 CC and accurate detection and/or identification of nucleic acids with low
 CC incidence of false positive results.
 XX
 SQ Sequence 56 AA;
 Query Match 27.7%; Score 101.5; DB 8; Length 56;
 Best Local Similarity 55.9%; Pred. No. 0.018;
 Matches 33; Conservative 0; Mismatches 21; Indels 5; Gaps 1;
 QY 15 AEAAKAEAKYKAEAKKAEAKKAEAKKAEAKKAEAKKAEAKKAEAKKAEAK 73
 DB 2 AAAAAKAAAAKAAAAKAAAAKAAAAKAAAAKAAAAKAAAAKAAAAKAAAA 55
 RESULT 9
 ADO04487
 ID ADO04487 standard; protein; 60 AA.
 XX
 AC ADO04487;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Sea urchin histone H1 variant protein.
 XX
 KW Macroscopic membrane; cell growth; EAK16; Z-DNA binding protein; zuotin;
 KW medical product; suture; artificial skin; internal lining;
 KW slow-diffusion drug delivery system; protein-type drug; erythropoietin;
 KW haemoglobin; insulin; cell adhesion; cell migration; Alzheimer's disease;
 KW scrapie infection; sea urchin; histone; H1; variant.
 XX
 OS Arbacia punctulata.
 XX
 XX US2004087013-A1.
 PN
 XX 06-MAY-2004.
 PD
 XX 17-MAR-2003; 2003US-00390472.
 PF
 XX 28-DEC-1992; 92US-00973326.
 PR 22-AUG-1994; 94US-00292284.
 PR 26-MAR-1997; 97US-00824515.
 XX
 XX (HOLM/) HOLMES T.
 PA (ZHAN/) ZHANG S.
 PA (RICH/) RICH A.
 PA (DIPE/) DIPERSIO C M.
 PA (LOCK/) LOCKSHIN C.

XX Holmes T, Zhang S, Rich A, Dipersio CM, Lockshin C;
 XX WPI; 2004-356208/33.
 XX Novel EAK16 protein incorporated into macroscopic membranes, useful in
 PT biomaterial applications such as medical products, artificial skin or
 PT internal linings, slow-diffusion drug delivery systems for in vitro cell
 PT growth.
 XX Example 5; SEQ ID NO 16; 56pp; English.
 XX The invention relates to a method for in vitro cell culture which
 CC involves adding a macroscopic membrane that is formed by self-assembly of
 CC amphiphilic peptide in an aqueous solution containing monovalent metal
 CC cations to a cell culture medium comprising cells, thus forming a
 CC membrane/culture mixture, maintaining the mixture under conditions
 CC sufficient for cell growth. The invention also relates to EAK16 peptide
 CC derived from yeast Z-DNA binding protein (zucotin). Zucotin incorporated
 CC into the macroscopic membranes are useful in biomaterial applications
 CC such as medical products (e.g., sutures), artificial skin or internal
 CC linings, slow-diffusion drug delivery systems supports for in vitro cell
 CC growth or culture and support for artificial tissue for in vivo use, as
 CC slow-diffusion drug delivery vehicle for delivering protein-type drugs
 CC e.g., erythropoietin, synthetic haemoglobin, insulin, etc., useful as
 CC conductive biopolymer for culturing cell monolayers, for promoting cell
 CC adhesion and migration, useful as experimental models for Alzheimer's
 CC disease and scrapie infection. The present sequence is sea urchin histone
 CC H1 variant protein. This sequence is used to illustrate the method of the
 CC invention.
 XX Sequence 60 AA;
 XX Query Match 27.7%; Score 101.5; DB 8; Length 60;
 XX Best Local Similarity 48.3%; Pred. No. 0.02;
 XX Matches 29; Conservative 7; Mismatches 23; Indels 1; Gaps 1;
 QY 2 KKYAKKEKAYAKAEKAAK-KAEAKAYKAAEAKKAAEAKKAAEAKKAAEAKKAAEAK 60
 DB 1 KAAAKRAALAKKAAAKKAAAKKAAKPKKAAKAAKAAKPKKAAKAAKPKKAAKPKK 60
 RESULT 10
 ADS15345
 ID ADS15345 standard; protein; 60 AA.
 XX ADS15345;
 AC ADS15345;
 DT 16-DEC-2004 (first entry)
 XX Yeast zucotin homologue sea urchin H1 delta.
 XX cell culture; macroscopic membrane; amphiphilic peptide; biomaterial;
 KW slow-diffusion drug delivery system; artificial skin; separation matrix;
 KW Alzheimer's disease; scrapie; liver cirrhosis; kidney amyloidosis;
 KW protein conformational disease; yeast; DNA binding protein; zucotin;
 KW sea urchin; H1 delta.
 XX Paracentrotus lividus.
 OS US6800481-B1.
 PN 05-OCT-2004.
 XX 26-MAR-1997; 97US-00824513.
 XX 28-DEC-1992; 92US-00973326.
 PR 22-AUG-1994; 94US-00293284.
 XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
 PA Holmes T, Zhang S, Rich A, Dipersio CM, Lockshin C;
 PI WPI; 2004-356208/33.
 XX

DR WPI; 2004-707224/69.
 XX Culturing cells, in vitro, by adding macroscopic membrane formed by self-
 PT assembly of amphiphilic peptides and monovalent metal cations, to form
 PT culture mixture, and maintaining culture mixture under conditions for
 PT cell growth.
 XX Example 5; SEQ ID NO 16; 50pp; English.
 XX The invention describes a method of culturing (M1) cells, in vitro. The
 CC cell culture involves adding a macroscopic membrane which is formed by
 CC self-assembly of amphiphilic peptides in an aqueous solution containing
 CC monovalent metal cations, where the peptides have alternating hydrophobic
 CC and hydrophilic amino acids and are complementary and structurally
 CC compatible, to a cell culture medium comprising cells, thus forming a
 CC membrane/culture mixture, and maintaining the mixture under conditions
 CC sufficient for cell growth. (M1) is useful for culturing a macroscopic
 CC membrane utilised in biomaterial applications e.g., slow-diffusion drug
 CC delivery systems, artificial skin or separation matrices, or as
 CC experimental models for Alzheimer's disease and scrapie infection e.g.,
 CC liver cirrhosis, kidney amyloidosis, or other protein conformational
 CC diseases. (M1) enables in vitro culturing of macroscopic membrane that is
 CC stable in aqueous solution, serum and ethanol, highly resistant to heat,
 CC alkaline and acidic pH, chemical denaturants and proteolytic digestion,
 CC and is non-cytotoxic. This is the amino acid sequence of a region found
 CC in sea urchin histone H1 delta which is homologous to yeast DNA binding
 CC protein zucotin from which amphiphilic peptides capable of forming
 CC membrane can be isolated.
 XX Sequence 60 AA;
 XX Query Match 27.7%; Score 101.5; DB 8; Length 60;
 XX Best Local Similarity 48.3%; Pred. No. 0.02;
 XX Matches 29; Conservative 7; Mismatches 23; Indels 1; Gaps 1;
 QY 2 KKYAKKEKAYAKAEKAAK-KAEAKAYKAAEAKKAAEAKKAAEAKKAAEAKKAAEAK 60
 DB 1 KAAAKRAALAKKAAAKKAAAKKAAKPKKAAKAAKAAKPKKAAKAAKPKKAAKPKK 60
 RESULT 11
 AAR28871
 ID AAR28871 standard; peptide; 46 AA.
 XX AAR28871;
 AC AAR28871;
 XX 25-MAR-2003 (revised)
 DT 23-MAR-1993 (first entry)
 XX High affinity macrophage mannose receptor ligand compound #9.
 DE glycopeptide; mannose; mannosylated; glycosylated; mannose receptor;
 KW macrophages; monocytes; destroy; cytotoxicity; label; image; alter;
 KW macrophage processing of antigen; MHC restriction; inflammation;
 KW inflammatory diseases; macrophage secretory products; Crohn's disease;
 KW legionnaires disease; mononuclear phagocytes; HIV; AIDS;
 KW lysosomal storage diseases; Gaucher's disease; asthma;
 KW alveolar macrophages metastasis; systemic macrophages; deliver;
 KW antigenic peptides; prevent transplant rejection; organ transplantation;
 KW antitumour agents; cancer; toxins.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 PH Modified-site 1
 FT /note= "opt may have mannose, fucose, glucose or N-Ac-
 FT glucosamine. May also have non interfering substituents."
 FT Modified-site 4
 FT /note= "opt may have mannose, fucose, glucose or N-Ac-
 FT glucosamine."
 FT Modified-site 7
 FT /note= "opt may have mannose, fucose, glucose or N-Ac-
 FT glucosamine."
 FT

FT	Modified-site	10	/note= "opt may have mannose, fucose, glucose or N-Ac-glucosamine."
FT		13	
FT	Modified-site	16	/note= "opt may have mannose, fucose, glucose or N-Ac-glucosamine."
FT		19	
FT	Modified-site	22	/note= "opt may have mannose, fucose, glucose or N-Ac-glucosamine."
FT		25	
FT	Modified-site	28	/note= "opt may have mannose, fucose, glucose or N-Ac-glucosamine."
FT		31	
FT	Modified-site	34	/note= "opt may have mannose, fucose, glucose or N-Ac-glucosamine."
FT		37	
FT	Modified-site	40	/note= "opt may have mannose, fucose, glucose or N-Ac-glucosamine."
FT		43	
FT	Modified-site	46	/note= "opt may have mannose, fucose, glucose or N-Ac-glucosamine."
FT			/note= "opt may have mannose, fucose, glucose or N-Ac-glucosamine. May also have non interfering substsits."
XX			
PN	W09219248-A1.		
XX			
PD	12-NOV-1992.		
XX			
XX	01-MAY-1992;	92WO-US003609.	
XX			
PR	03-MAY-1991;	91US-00694983.	
XX			
PA	(UNIW) UNIV WASHINGTON.		
XX			
PI	Stahl PD;		
XX			
XX			
DR	WFI; 1992-398516/48.		
XX			
PT	New high affinity mannose receptor ligand cpds. - for treating diseases mediated by macrophage activity e.g. asthma, inflammatory diseases and infectious diseases, e.g. HIV.		
PT			
XX			
PS	Claim 3; Page 21; 32pp; English.		
XX			
CC	This compound represents a glycopeptide effective in inhibiting the binding of labelled mannosylated BSA to mannose receptors. Mannose receptors are uniquely found on macrophages and not on monocytes.		
CC	Glycopeptides such as this provide a mechanism to target macrophages specifically, to image, label, destroy or otherwise alter their antigen processing function. In addition they can be conjugated to solid supports and used to purify mannose receptors from a variety of sources. They are useful in the treatment of inflammatory diseases driven by macrophage secretory products eg. Crohn's disease; infectious diseases in which macrophages harbour replicating infectious agents eg. Legionnaires disease; viral infections involving mononuclear phagocytes eg. HIV and lysosomal storage diseases, in which macrophages are principally involved eg. Gaucher's disease; asthma mediated by alveolar macrophages; and in		

CC controlling metastasis, mediated by systemic macrophages. The peptides
CC can also be used to deliver antigenic peptides as conjugates to a
CC macrophage to marshal an immune response; also self peptides to prevent
CC tissue transplant rejection. (Updated on 25-MAR-2003 to correct PN
XX field.)
SQ Sequence 46 AA;

Query Match 27.2%; Score 99.5; DB 2; Length 46;
Best Local Similarity 58.9%; Pred. No. 0.023;
Matches 33; Conservative 3; Mismatches 9; Indels 11; Gaps

QY 14 KAKKAAPAFKAYKAAEAKKKAKAEAKKYAKAAKAEKKFYAAAEAKYKAERAKAA 69
|| ||||| ||| |||| | ||| ||||| | ||| : |||||
Db 1 KAAKAAK--AAKAAKAAKAAKAAK-----AKAAKAAK---AAKAAKAAKAAKAA 45

RESULT 12
ADE10646
ID ADE10646 standard; protein; 75 AA.
XX AC
XX AC
XX AC
DT 29-JAN-2004 (first entry)
XX
DE Structurally biased random peptide library related protein seqid 53.
XX
XX fusion nucleic acid library; scaffold protein; bioactive peptide;
KW phenotype change; cell morphology; cell growth; cell viability;
KW cell adhesion; cellular density; cancer; tumour; apoptosis; cell death;
KW loss of cell division; decreased cell growth; brca-1; brca-2;
KW tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC;
KW Dröschilia discs-large; Dlg; cardiovascular; neurobiology; bone biology
KW skin biology; cosmeceutical; endocrinology; infectious disease;
KW drug toxicity; drug resistance; inflammation; allergic response.
XX Synthetic.

OS
XX
XX US2003143562-A1.
PN
XX
XX 31-JUL-2003.
PD
XX
XX 20-JUN-2002; 2002US-00177725.
PF
XX
XX 08-OCT-1998; 98US-00169015.
PR
XX
XX 08-OCT-1999; 99US-00415765.
XX
XX (RIGE-) RIGEL PHARM INC.
PA
XX
XX Anderson D, Peelle BR, Bogenberger JM;
PI
XX WPI; 2003-829786/77.
DR
XX
XX Novel library of fusion nucleic acids each of which has fused first and
PT second nucleic acids encoding scaffold protein and library peptide havin
FT alpha helical biasing sequence, respectively, useful in screening
PT methods.
XX
XX Example 6; SEQ ID NO 53; 110pp; English.
PS
XX
XX The invention describes a library (I) of fusion nucleic acids, where ea
CC fusion nucleic acid comprises a first nucleic acid (N1), encoding a
CC scaffold protein sequence; and a second nucleic acid (N2), encoding a
CC library peptide sequence comprising an alpha helical biasing sequence;
CC where N1 is fused to N2. Disclosed is a method for screening bioactive
CC peptides conferring a change in specific phenotype such as cell
CC morphology, cell growth, cell viability, adhesion to substrates or other
CC cells, and cellular density; changes in the expression of one or more
CC RNAs; proteins, lipids, hormones, cytokines, or other molecules; change
CC in the equilibrium state (i.e., half-life) or one or more RNAs; protein
CC lipids, hormones, cytokines, or other molecules; etc. The bioactive
CC peptide identified by above mentioned method is used to generate more
CC candidate peptides and to identify target molecules, i.e. the molecule

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```
Db 61 YKAEAAKAAKEAAEAYEA 77
RESULT 2
US-10-792-311-5
; Sequence 5, Application US/10792311
; Publication No. US20050038233A1
; GENERAL INFORMATION:
; APPLICANT: Gad, Alexander
; APPLICANT: Lis, Doris
; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
; TITLE OF INVENTION: AND FOR THERAPEUTIC USE
; FILE REFERENCE: 2609/60807-A-PCT-US
; CURRENT APPLICATION NUMBER: US/10/792,311
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/09/816,989
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/101,693
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22402
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-10-792-311-5
Query Match 100.0%; Score 366; DB 17; Length 77;
Best Local Similarity 100.0%; Pred. No. 7.1e-25;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AKKYAKKEKAYAKKAEAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKYAKAAKAEKKYAAAEAK 60
Db 1 AKKYAKKEKAYAKKAEAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKYAKAAKAEKKYAAAEAK 60
Qy 61 YKAEAAKAAKEAAEAYEA 77
Db 61 YKAEAAKAAKEAAEAYEA 77
RESULT 3
US-09-816-989A-4
; Sequence 4, Application US/09816989A
; Patent No. US20020115103A1
; GENERAL INFORMATION:
; APPLICANT: Gad, Alexander
; APPLICANT: Lis, Doris
; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
; TITLE OF INVENTION: AND FOR THERAPEUTIC USE
; FILE REFERENCE: 2609/60807-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/816,989A
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/101,693
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22402
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-4
Query Match 77.2%; Score 282.5; DB 9; Length 66;
Best Local Similarity 84.4%; Pred. No. 1e-17;
Matches 65; Conservative 0; Mismatches 1; Indels 11; Gaps 2;
Qy 61 YKAEAAKAAKEAAEAYEA 77
Db 61 YKAEAAKAAKEAAEAYEA 77
RESULT 4
US-10-792-311-4
; Sequence 4, Application US/10792311
; Publication No. US20050038233A1
; GENERAL INFORMATION:
; APPLICANT: Gad, Alexander
; APPLICANT: Lis, Doris
; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
; TITLE OF INVENTION: AND FOR THERAPEUTIC USE
; FILE REFERENCE: 2609/60807-A-PCT-US
; CURRENT APPLICATION NUMBER: US/10/792,311
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/09/816,989
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/101,693
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22402
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-10-792-311-4
Query Match 77.2%; Score 282.5; DB 17; Length 66;
Best Local Similarity 84.4%; Pred. No. 1e-17;
Matches 65; Conservative 0; Mismatches 1; Indels 11; Gaps 2;
Qy 1 AKKYAKKEKAYAKKAEAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKYAKAAKAEKKYAAAEAK 60
Db 1 AKKYAKKEKAYAKKAEAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKYAKAAKAEKKYAAAEAK 49
Qy 61 YKAEAAKAAKEAAEAYEA 77
Db 50 YKAEAAKAAKEAAEAYEA 66
RESULT 5
US-09-816-989A-3
; Sequence 3, Application US/09816989A
; Patent No. US20020115103A1
; GENERAL INFORMATION:
; APPLICANT: Gad, Alexander
; APPLICANT: Lis, Doris
; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
; TITLE OF INVENTION: AND FOR THERAPEUTIC USE
; FILE REFERENCE: 2609/60807-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/816,989A
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/101,693
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22402
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-3
Query Match 77.2%; Score 282.5; DB 9; Length 66;
Best Local Similarity 84.4%; Pred. No. 1e-17;
Matches 65; Conservative 0; Mismatches 1; Indels 11; Gaps 2;
Qy 61 YKAEAAKAAKEAAEAYEA 77
Db 50 YKAEAAKAAKEAAEAYEA 66
```



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; APPLICANT: YAWAKAWA, Mineo
; TITLE OF INVENTION: CONTROLLED ALIGNMENT OF NANO-BARCODES ENCODING SPECIFIC INFORMATION
; FILE REFERENCE: INTEL1310-1(P14240X)
; CURRENT APPLICATION NUMBER: US/10/667,004
; PRIOR FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US 10/251,152
; PRIOR FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-667-004-20

Query Match          30.5%; Score 111.5; DB 16; Length 63;
Best Local Similarity 56.2%; Pred. No. 0.0065;
Matches 36; Conservative 0; Mismatches 23; Indels 5; Gaps 1;

QY 10 AYAKKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 69
Db 4 AAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 58
QY 70 AKAA 73
Db 59 AAAA 62

RESULT 10
US-09-816-989A-1
; Sequence 1, Application US/09816989A
; Patent No. US20020115103A1
; GENERAL INFORMATION:
; APPLICANT: Gad, Alexander
; APPLICANT: Lis, Doris
; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
; FILE REFERENCE: 2609/60807-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/816,989A
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/101,693
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22402
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-1

Query Match          28.6%; Score 104.5; DB 9; Length 35;
Best Local Similarity 65.8%; Pred. No. 0.014;
Matches 25; Conservative 4; Mismatches 6; Indels 3; Gaps 1;

QY 40 AKYAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 77
Db 1 AKKYAKKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 35

RESULT 11
US-10-792-311-1
; Sequence 1, Application US/10792311
; Publication No. US20050038233A1
; GENERAL INFORMATION:
; APPLICANT: Gad, Alexander
; APPLICANT: Lis, Doris
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; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
; FILE REFERENCE: 2609/60807-A-PCT-US
; CURRENT APPLICATION NUMBER: US/10/792,311
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/09/816,989
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/101,693
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22402
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-10-792-311-1

Query Match          28.6%; Score 104.5; DB 17; Length 35;
Best Local Similarity 65.8%; Pred. No. 0.014;
Matches 25; Conservative 4; Mismatches 6; Indels 3; Gaps 1;

QY 40 AKYAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 77
Db 1 AKKYAKKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 35

RESULT 12
US-10-390-472-16
; Sequence 16, Application US/10390472
; Publication No. US20040087013A1
; GENERAL INFORMATION:
; APPLICANT: Holmes, Todd
; APPLICANT: Zhang, Shuguang
; APPLICANT: Rich, Alexander
; APPLICANT: DiPersio, C. Michael
; APPLICANT: Lockshin, Curtis
; TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES THEREFOR
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSER: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/390,472
; FILING DATE: 17-Mar-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,284
; FILING DATE: 22-AUG-1994
; APPLICATION NUMBER: 07/973,326
; FILING DATE: 28-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: MIT-6008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 16:
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```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-390-472-16

Query Match      27.7%; Score 101.5; DB 15; Length 60;
Best Local Similarity 48.3%; Pred. No. 0.045;
Matches 29; Conservative 7; Mismatches 23; Indels 1; Gaps 1;

Qy 2 KKYAKKEKAYAKAEKAAK-KAEAKYKAAKAKKAKAEKAKYKAAKAEKKEKVEYAAAEAK 60
Db 1 KAAAKRYAALAKKAAAKKAAAKKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAK 60

RESULT 13
US-10-038-854-235
; Sequence 235, Application US/10038854
; Publication No. US20040022781A1
; GENERAL INFORMATION:
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Li, Li
; APPLICANT: Wolenc, Adam R
; APPLICANT: Vernet, Corine
; APPLICANT: Eisen, Andrew J
; APPLICANT: Liu, Xiaohong
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shimkets, Richard A
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spaderna, Steven K
; APPLICANT: Gorman, Linda
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Gangolli, Esha A
; APPLICANT: Guo, Xiaojia S
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Rastelli, Luca
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc
; APPLICANT: Burgess, Catherine E
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Ellerman, Karen
; APPLICANT: Smithson, Glenna
; APPLICANT: Millet, Isabelle
; APPLICANT: MacDougall, John R
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-230
; CURRENT APPLICATION NUMBER: US/10/038,854
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 60/258,928
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: 60/259,415
; PRIOR FILING DATE: 2001-01-02
; PRIOR APPLICATION NUMBER: 60/279,832
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,833
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,447
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/286,683
; PRIOR FILING DATE: 2001-04-25

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 411
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 235
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-854-235

Query Match      27.6%; Score 101; DB 15; Length 75;
Best Local Similarity 43.2%; Pred. No. 0.063;
Matches 32; Conservative 9; Mismatches 29; Indels 4; Gaps 2;

Qy 1 AKKYAKKEKAYAKAEKAAKAEKAYKAAEAKKKAKAEAKKYKAAKA-EKKEYAARAE 59
Db 3 AKETADSAKSEAKDAKAD---KAEAKDAKAEKAEAKDAKAEKAKGAKGAKGAKGAKGAKGAK 59

Qy 60 KYKAAEAAKAAAEK 73
Db 60 KEKAEAKDKASDA 73

RESULT 14
US-10-038-854-236
; Sequence 236, Application US/10038854
; Publication No. US20040022781A1
; GENERAL INFORMATION:
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Li, Li
; APPLICANT: Wolenc, Adam R
; APPLICANT: Vernet, Corine
; APPLICANT: Eisen, Andrew J
; APPLICANT: Liu, Xiaohong
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shimkets, Richard A
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spaderna, Steven K
; APPLICANT: Gorman, Linda
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Gangolli, Esha A
; APPLICANT: Guo, Xiaojia S
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Rastelli, Luca
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc
; APPLICANT: Burgess, Catherine E
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glenna
; APPLICANT: Millet, Isabelle
; APPLICANT: MacDougall, John R
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-230
; CURRENT APPLICATION NUMBER: US/10/038,854
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 60/258,928
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: 60/259,415
; PRIOR FILING DATE: 2001-01-02
; PRIOR APPLICATION NUMBER: 60/259,785
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 60/269,814
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/279,832
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,833
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,863
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/283,889
```



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/ AFFILIATION: macdougall, john k
/
/ TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
/
/ FILE REFERENCE: 21402-230
/
/ CURRENT APPLICATION NUMBER: US/10/038,854
/
/ CURRENT FILING DATE: 2003-01-22
/
/ PRIOR APPLICATION NUMBER: 60/258,928
/
/ PRIOR FILING DATE: 2000-12-29
/
/ PRIOR APPLICATION NUMBER: 60/259,415
/
/ PRIOR FILING DATE: 2001-01-02
/
/ PRIOR APPLICATION NUMBER: 60/259,785
/
/ PRIOR FILING DATE: 2001-01-04
/
/ PRIOR APPLICATION NUMBER: 60/269,814
/
/ PRIOR FILING DATE: 2001-02-20
/
/ PRIOR APPLICATION NUMBER: 60/279,832
/
/ PRIOR FILING DATE: 2001-03-29

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Result No.	Score	Query		Length	DB	ID	Description
		Match	✦				
1	366	100.0	77	4	US-09-405-743A-5	Sequence 5, Appli	
2	366	100.0	77	4	US-09-816-989A-5	Sequence 5, Appli	
3	282.5	77.2	66	4	US-09-405-743A-4	Sequence 4, Appli	
4	282.5	77.2	66	4	US-09-816-989A-4	Sequence 4, Appli	
5	245.5	67.1	56	4	US-09-405-743A-3	Sequence 3, Appli	
6	245.5	67.1	56	4	US-09-816-989A-3	Sequence 3, Appli	
7	131	35.8	45	4	US-09-405-743A-2	Sequence 2, Appli	
8	131	35.8	45	4	US-09-816-989A-2	Sequence 2, Appli	
9	119.5	32.7	56	3	US-08-993-008A-6	Sequence 6, Appli	
10	106.5	29.1	48	3	US-08-993-008A-5	Sequence 5, Appli	
11	104.5	28.6	35	4	US-09-405-743A-1	Sequence 1, Appli	
12	104.5	28.6	35	4	US-09-816-989A-1	Sequence 1, Appli	
13	101.5	27.7	60	1	US-08-346-849-16	Sequence 16, Appl	
14	101.5	27.7	60	2	US-08-293-284A-16	Sequence 16, Appl	
15	101.5	27.7	60	4	US-08-998-300-16	Sequence 16, Appl	
16	101.5	27.7	60	4	US-08-824-513-16	Sequence 16, Appl	
17	92	25.1	61	3	US-08-995-172-6	Sequence 6, Appli	
18	92	25.1	61	3	US-08-995-172-7	Sequence 7, Appli	
19	92	25.1	61	4	US-09-221-050-7	Sequence 7, Appli	
20	92	25.1	61	4	US-09-247-054-11	Sequence 11, Appl	
21	89	24.3	61	1	US-08-346-849-17	Sequence 17, Appl	
22	89	24.3	61	2	US-08-293-284A-17	Sequence 17, Appl	
23	89	24.3	61	4	US-08-998-300-17	Sequence 17, Appl	
24	89	24.3	61	4	US-08-824-513-17	Sequence 17, Appl	
25	89	24.3	69	4	US-09-107-433-4761	Sequence 4761, Ap	
26	86	23.5	59	3	US-08-460-890A-60	Sequence 60, Appl	
27	86	23.5	59	3	US-08-167-641C-60	Sequence 60, Appl	


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; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-4

Query Match          77.2%; Score 282.5; DB 4; Length 66;
Best Local Similarity 84.4%; Pred.No. 4.Se-20;
Matches 65; Conservative 0; Mismatches 0; Indels 11; Gaps :

QY      1 AKKYAKKEKAYAKAEKAACKAAEAKKAEAKYKAAAEAKKKAKAEAKKYAKAAKAEKKEYAAAAEAK
Db       1 AKKYAKEKEKAYAK-----AKKAEAK-----AKKAKAEAKKYAKAAKAEKKEYAAAAEAK
QY      61 YKAEAAAATAAAEAAYEA 77
Db       50 YKAEAAKAAAEAAAYEA 66

RESULT 5
US-09-405-743A-3
; Sequence 3, Application US/09405743A
; Patent No. 6514938
; GENERAL INFORMATION:
; APPLICANT: Yeda Research and Development Co., Ltd.
; TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
; FILE REFERENCE: 60807-A
; CURRENT APPLICATION NUMBER: US/09/405,743A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PEPTIDE
US-09-405-743A-3

Query Match          67.1%; Score 245.5; DB 4; Length 56;
Best Local Similarity 72.7%; Pred.No. 1.le-16;
Matches 56; Conservative 0; Mismatches 0; Indels 21; Gaps :

QY      1 AKKYAKKEKAYAKAEKAACKAAEAKKAEAKYKAAAEAKKKAKAEAKKYAKAAKAEKKEYAAAAEAK
Db       1 AKKYAKEKEKAYAKAEKAACKAAEAKKAEAKYKAAAEAKKK-----AEAK 39
QY      61 YKAEAAAATAAAEAAYEA 77
Db       40 YKAEAAKAAAEAAAYEA 56

RESULT 6
US-09-816-989A-3
; Sequence 3, Application US/09816989A
; Patent No. 6800287
; GENERAL INFORMATION:
; APPLICANT: Gad, Alexander
; APPLICANT: Lis, Doris
; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR
; TITLE OF INVENTION: AND FOR THERAPEUTIC USE
; FILE REFERENCE: 2609/60807-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/816,989A
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/101,693
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22402
; PRIOR FILING DATE: 1999-09-24

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; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-3

Query Match      67.1%; Score 245.5; DB 4; Length 56;
Best Local Similarity 72.7%; Pred. No. 1.1e-16;
Matches 56; Conservative 0; Mismatches 0; Indels 21; Gaps 1;

QY 1 AKKYAKKEKAYAKAEKAAKAEKAYKAAAEKAKKAAKAAKAEKKEYYAAAEAK 60
    |||||
DB 1 AKKYAKKEKAYAKAEKAAKAEKAYKAAAEKAKKAAKAAKAEKKEYYAAAEAK 60
    |||||
QY 61 YKAEAAKAAKAAEAAYEA 77
    |||||
DB 40 YKAEAAKAAKAAEAAYEA 56
    |||||

RESULT 7
US-09-405-743A-2
; Sequence 2, Application US/09405743A
; Patent No. 6514938
; GENERAL INFORMATION:
; APPLICANT: Yeda Research and Development Co., Ltd.
; TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
; FILE REFERENCE: 60807-A
; CURRENT APPLICATION NUMBER: US/09/405,743A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-405-743A-2

Query Match      35.8%; Score 131; DB 4; Length 45;
Best Local Similarity 50.6%; Pred. No. 4.8e-06;
Matches 39; Conservative 0; Mismatches 6; Indels 32; Gaps 3;

QY 1 AKKYAKKEKAYAKAEKAAKAEKAYKAAAEKAKKAAKAAKAEKKEYYAAAEAK 60
    |||||
DB 1 AKKYAKK-----AKAEK-----KKAYKAAAEKAAKAEY----- 29
    |||||
QY 61 YKAEAAKAAKAAEAAYEA 77
    |||||
DB 30 -KAAAEKAAKAAEAAYEA 45
    |||||

RESULT 8
US-09-816-989A-2
; Sequence 2, Application US/09816989A
; Patent No. 6800287
; GENERAL INFORMATION:
; APPLICANT: Gad, Alexander
; APPLICANT: Lis, Doris
; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
; FILE REFERENCE: 2609/60807-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/816,989A
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/101,693
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22402
; PRIOR FILING DATE: 1999-09-24

US-09-816-989A-2

Query Match      35.8%; Score 131; DB 4; Length 45;
Best Local Similarity 50.6%; Pred. No. 4.8e-06;
Matches 39; Conservative 0; Mismatches 6; Indels 32; Gaps 3;

QY 1 AKKYAKKEKAYAKAEKAAKAEKAYKAAAEKAKKAAKAAKAEKKEYYAAAEAK 60
    |||||
DB 1 AKKYAKK-----AKAEK-----KKAYKAAAEKAAKAEY----- 29
    |||||
QY 61 YKAEAAKAAKAAEAAYEA 77
    |||||
DB 30 -KAAAEKAAKAAEAAYEA 45
    |||||

RESULT 9
US-08-993-008A-6
; Sequence 6, Application US/08993008A
; Patent No. 6153596
; GENERAL INFORMATION:
; APPLICANT: Liotta, Dennis C.
; APPLICANT: Petros, John A.
; APPLICANT: Wey, Shlow-Jyi
; APPLICANT: Karr, Joan F.
; APPLICANT: Pohl, Jan
; TITLE OF INVENTION: Polycationic Oligomers
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,008A
; FILING DATE: 18-DEC-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/032,436
; FILING DATE: 18-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sullivan, Sally A.
; REGISTRATION NUMBER: 32,064
; REFERENCE/DOCKET NUMBER: 33-95
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-499-8080
; TELEFAX: 303-499-8089
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 56 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-993-008A-6

Query Match      32.7%; Score 119.5; DB 3; Length 56;

```


SECRET

MOLECULE TYPE: protein

RESULT 14
US-08-293-284A-16
; Sequence 16, Application US/08293284A
; Patent No. 5955343
; GENERAL INFORMATION:
; APPLICANT: Holmes, Todd
; APPLICANT: Zhang, Shuguang
; APPLICANT: Rich, Alexander
; APPLICANT: Dipersio, C. Michael
; APPLICANT: Lockshin, Curtis
; TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
; TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,284A
; FILING DATE: 22-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,326

A:Molecule type: mRNA
A:Residues: 1-85 <LIN>
A/Cross-references: UNIPROT:P02734
C/Superfamily: antifreeze protein
C/Keywords: antifreeze
F/1-21/Domain: signal sequence #status predicted <SIG>
F/22-85/Product: antifreeze protein 4 #status predicted <MAT>

Query Match 17.8%; Score 73; DB 1; Length 85;
Best Local Similarity 45.3%; Pred. No. 40;
Matches 29; Conservative 1; Mismatches 32; Indels 2; Gaps 1;

QY 23 EKAYKAAEAKKKAKAEKTKAKAKAEKKEKYAAAEKTKAKAEKAYKAEKAAKAAEA 82
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 11 DAKAVPAAAAADTASDAAA--AAAAATATAAAAAAATAATRAAAAAATAATAAKGAALTA 68

QY 83 AYE 86
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 69 ANAA 72

RESULT 6
S10544
Protamine phi-3.2 - California mussel
N/Alternate names: protamine PL-IV.2
C/Species: Mytilus californianus (California mussel)
C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C/Accession: S10544
R/Ausio, J.; McParland, R.
Eur. J. Biochem. 182, 569-576, 1989
A/Title: Sequence and characterization of the sperm-specific protein phi3 from Mytilus c
A/Reference number: S04941; MUID:89325302; PMID:2666130
A/Accession: S10544
A/Molecule type: protein
A:Residues: 1-45 <AUS>
A/Cross-references: UNIPROT:P11860
C/Superfamily: histone H1
C/Keywords: DNA binding; nucleus

Query Match 17.6%; Score 72; DB 2; Length 45;
Best Local Similarity 42.2%; Pred. No. 29;
Matches 19; Conservative 8; Mismatches 14; Indels 4; Gaps 1;

QY 1 AKKYAKEKAYAKKAEEAKKAEEAKAYKAAEKKAEEKKAAEKKYAK 45
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 3 AKGSRPKKTAVKK----SSSKAKKPSPKKKAAKKPAKKAOK 43

RESULT 7
QFB0
micro glutamic acid-rich protein - bovine
N/Alternate names: neurofilament triplet L protein (fragment)
C/Species: Bos primigenius taurus (cattle)
C/Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 22-Nov-1996
C/Accession: A02964
R/Isoe, T.; Okuyama, T.
FEBS Lett. 182, 389-392, 1985
A/Title: Brain micro glutamic acid-rich protein is the C-terminal endpiece of the neurofi
A/Reference number: A02964; MUID:85154567; PMID:3884373
A/Accession: A02964
A/Molecule type: protein
A:Residues: 1-82 <ISO>
C/Comment: This acidic protein, isolated from the cytosolic fraction of brain tissue, cor
C/Comment: The similarity of this sequence to part of the neurofilament triplet L protei
f the L protein.
C/Comment: Although there are, as yet, no known biological functions ascribed to this pr
to cytoplasmic neuronal transport occurring in the presence of calcium ion and possibly
C/Superfamily: cytoskeletal keratin
C/Keywords: brain; coiled coil; cytosol; intermediate filament
F/1-82/Domain: neurofilament triplet L protein tail subdomain b (fragment) <SIG>

Query Match 17.4%; Score 71; DB 1; Length 82;
Best Local Similarity 34.3%; Pred. No. 54;


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A;Residues: 1-69 <GLA>
A;Cross-references: UNIPROT:Q8Y506; GB:NC_003210; PIDN:CAD00350.1; PID:g16411742; GSPDB:
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo2272

Query Match          14.9%; Score 61; DB 2; Length 69;
Best Local Similarity 34.5%; Pred. No. 2.4e+02;
Matches 20; Conservative 7; Mismatches 31; Indels 0; Gaps 0;

QY      16   EKAAKAEAKYKAAEKKKAKAEAKYKAKAEKKEVAAAAEKYKAAEAACKYKAE 73
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||
Db       3   KKTSDAQLKANKAWQDKNKEHANYLKSARSFIKKKATLEDLELEIAIKQKTE 60

RESULT 15
S58143
Gene 14 protein - phase SPP1
C;Species: phage SPP1
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C;Accession: S58143; T42284
R;Becker, B.; Gassel, M.; Tavares, P.; Lurz, R.; Alonso, J.C.
submitted to the EMBL Data Library July 1995
A;Description: Head morphogenesis of the Bacillus subtilis bacteriophage SPPl.
A;Reference number: S58137
A;Accession: S58143
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-58 <BEC>
A;Cross-references: UNIPROT:Q38583; EMBL:X89721; NID:g1052805; PIDN:CAA61871.1; PID:g1052805
R;Alonso, J.C.; Luder, G.; Stiege, A.C.; Chai, S.; Weise, F.; Trautner, T.A.
Gene 204, 201-212, 1997
A;Title: The complete nucleotide sequence and functional organization of Bacillus subtilis
A;Reference number: 222137; UID:98094274; PMID:9434185
A;Accession: T42284
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-58 <ALO>
A;Cross-references: EMBL:X97918; PIDN:CAA66545.1

Query Match          14.7%; Score 60; DB 2; Length 58;
Best Local Similarity 39.6%; Pred. No. 2.5e+02;
Matches 19; Conservative 7; Mismatches 20; Indels 2; Gaps 2;

QY      1   AKKYAKEKAYAKAEKAAKAEKAAKAEKAAKAEKAAKAEKAAKAEKAAKAEKAAK 48
       ||:::||:::||::||::||::||::||::||::||::||::||::||::||
Db     11   AKQREEREERARKAEE-EKASEKRQGAQ-KPKKDSEKSTRKPCK 56

Search completed: June 3, 2005, 11:34:54
Job time : 38 secs

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Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	116	28.4	81	2	Q9N6L9	trypanosoma
2	112	27.4	81	2	Q9NPP6	trypanosoma
3	111.5	27.3	76	2	Q9N6J8	trypanosoma
4	110.5	27.0	68	2	Q26907	trypanosoma
5	107.5	26.3	76	2	Q9NFFJ4	trypanosoma
6	104.5	25.6	71	2	Q9N6K5	trypanosoma
7	103.5	25.3	82	2	Q87W81	pseudomonas
8	102	24.9	71	2	Q9N6J8	trypanosoma
9	100.5	24.6	71	2	Q9N6K0	trypanosoma
10	100	24.4	85	2	Q9N668	trypanosoma
11	97.5	23.8	76	2	Q9NFFJ2	trypanosoma
12	97.5	23.8	76	2	Q9NFFJ6	trypanosoma
13	97.5	23.8	80	1	H161 TRYCR	trypanosoma
14	97.5	23.8	85	2	Q26777	trypanosoma
15	97	23.7	76	2	Q9N6N7	trypanosoma
16	97	23.7	76	2	Q9NFF1	trypanosoma
17	97	23.7	83	2	Q9N5UN6	trypanosoma
18	96.5	23.6	75	2	Q9NFK0	trypanosoma
19	94	23.0	74	1	H1C8 TRYCR	trypanosoma
20	93.5	22.9	76	2	Q9N6T0	trypanosoma
21	93.5	22.9	78	2	Q9N5UN5	trypanosoma
22	89.5	21.9	80	2	Q9N6S6	trypanosoma
23	85.5	20.9	61	2	Q9NFFJ5	trypanosoma
24	85	20.8	60	2	Q9U3W3	caenorhabditis
25	85	20.8	66	2	Q9NFFJ3	trypanosoma
26	84.5	20.7	61	2	Q9NFFJ7	trypanosoma
27	84	20.5	85	2	Q7RLP9	plasmidium
28	82	20.0	62	2	Q17536	caenorhabditis
29	81.5	19.9	66	2	Q95QZ0	caenorhabditis
30	81	19.8	78	1	PH10 HOLTU	holothuria
31	79.5	19.4	78	2	O8KF25	chlorobium


```

Db      58 PKKVAPK---KVAGKKAQAKKA 76
|||||:|

RESULT 4
Q26907 PRELIMINARY; PRT; 68 AA.
AC Q26907;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cytoplasmic repetitive antigen (CRA) protein (Fragment).
OS Trypanosoma cruzi.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma
OC NCBI_TaxID=5693;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89364992; PubMed=2475776; DOI=10.1016/0166-6851(89)90115-1;
RA Lafaille J.U., Lins J., Krieger M.A., Souto-Padron T., de Souza W.
RA Goldenberg S.;
RT "Structure and expression of two Trypanosoma cruzi genes encoding
RT antigenic proteins bearing repetitive epitopes.";
RL Mol. Biochem. Parasitol. 35:127-136(1989).
DR EMBL; J04016; AAA30177.1; -.
DR InterPro; IPR009761; CRA_rpt.
DR Pfam; PF07046; CRA_rpt; 2.
FT NON TER 1
FT NON TER 68
FT NON TER 68
SQ SEQUENCE 68 AA; 7208 MW; ED6CF031B3DE7D1F CRC64;

Query Match 27.0%; Score 110.5; DB 2; Length 68;
Best Local Similarity 42.1%; Pred. No. 0.4;
Matches 32; Conservative 12; Mismatches 23; Indels 9; Gaps

QY 3 KVAKKEKAVAKAEKAAKAEKAVKAAEAKKKAKAEKAKYAKAEKKEKVEAAAEKAVK
DB 1 RVAAEK--QRAEATKVAAEKQKAAEATKVAAEKQRAEATKVAEAE-----KQK
QY 63 AEAAKKYAKAEAKAA 78
DB 52 AAETKVAAEKQKAA 67

RESULT 5
Q9NFJ4 PRELIMINARY; PRT; 76 AA.
AC Q9NFJ4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Histone H1.
DE Stone H1.
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma
OC NCBI_TaxID=5702;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=427;
RA Grueter E.;
RA Thesis (2000), Department of Parasitology, Institute of Zoology,
RL SWITZERLAND.
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=427;
RA Grueter E., Betschart B.;
RA Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ287607; CAB76192.1; -.
SQ SEQUENCE 76 AA; 7505 MW; 83BE50D89F1BED8F CRC64;

Query Match 26.3%; Score 107.5; DB 2; Length 76;
Best Local Similarity 48.8%; Pred. No. 0.72;
Matches 40; Conservative 3; Mismatches 32; Indels 7; Gaps

```


RA	Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H., Nelson W.C., Davidsons T.M., Zafar N., Zhou L., Liu J., Yuan Q., Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J., Utterback T.R., Van Aken S.E., Feldblyum T.V., D'Acenzio M., Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K., Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X., Bender C.L., White O., Frazer C.M., Collmer A.;
RA	"The complete genome sequence of the Arabidopsis and tomato pathogen RT Pseudomonas syringae pv. tomato DC3000.";
RT	Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
DR	EMBL; AF016872; AA058119.1; --
DR	TIGR; PSPOT4673; --
KW	Complete proteome; Hypothetical protein.
SQ	SEQUENCE 82 AA; 8888 MW; 3826079B39FAD75C CRC64;
Query Match	25.3%; Score 103.5; DB 2; Length 82;
Best Local Similarity	39.5%; Pred. No. 1.5;
Matches 30; Conservative 10; Mismatches 35; Indels 1; Gaps	
QY	6 KKEKAYAKAEKAACKAAYKAAEKKKAKAEKKYAKAKAEKKYAAAEAKYKAAE 64
Dd	: : : : : : : : : : :
Dd	6 KKSKEASAKSODLKXKASPAPKSEAAATLSKSEKKDKKKDAEPKK-AAKADSPEK 64
QY	66 AKAYAKAEAAKAAAKE 81
Dd	: : : : : : : : : :
Dd	65 AKSKDSEKAERPAKK 80
RESULT 8	
ID Q9NFJ8	PRELIMINARY; PRT; 71 AA.
ID Q9NFJ8	
AC Q9NFJ8	
DT 01-OCT-2000	(TrEMBLrel. 15, Created)
DC 01-OCT-2000	(TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002	(TrEMBLrel. 22, Last annotation update)
DE Histone H1.	
OS Name=H1A71;	
GN Trypanosoma brucei gambiense.	
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.	
OX NCBI_TaxID=31285;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=STIB 755;	
RA Grueter E., Betschart B.;	
RL Thesis (2000), Department of Parasitology, Institute of Zoology.	
RL SWITZERLAND.	
RN [2]	
RP SEQUENCE FROM N.A.	
RC STRAIN=STIB 755;	
RA Grueter E., Betschart B.;	
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.	
RL EMBL; AJ287594; CAB76176.1;	
SQ SEQUENCE 71 AA; 7019 MW; 6C7DED4F3E75D8C4 CRC64;	
Query Match	24.9%; Score 102; DB 2; Length 71;
Best Local Similarity	48.7%; Pred. No. 1.7;
Matches 38; Conservative 29; Indels 8; Gaps	
QY	1 AKKYAKKEKAYAKAEKAAKGAAGAEKAYKAAEAEEKKAKAEKKYAKAAAEKKEYAAAAEK 60
Dd	: : : : : : : : : : :
Dd	2 AKASAAPKKAVAKGA--APKKAVAK--KAAAPKAVAKKAAAPKVAKKAAAPKKAAPKVA 64
QY	61 YKAAEAKKAYKAAEAKAA 78
Dd	: : : : : : : : : :
Dd	58 PKKVAGKGA----AAKKA 71
RESULT 9	
ID Q9N6KO	PRELIMINARY; PRT; 71 AA.
ID Q9N6KO	
AC Q9N6KO	
DT 01-OCT-2000	(TrEMBLrel. 15, Created)


```

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
GN Histone H1.
OS Trypanosoma brucei brucei;
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5702;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=TREU 927/4;
RA Grueter E.; Betschart B.;
RL Thesis (2000), Department of Parasitology, Institute of Zoology,
RL SWITZERLAND.
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=TREU 927/4;
RA Grueter E.; Betschart B.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ400891; CAB90839.1; -.
DR EMBL; AJ287600; CAB76185.1; -.
SQ SEQUENCE 71 AA; 7005 MW; 478C7B6994847C80 CRC64;

Query Match 24.6%; Score 100.5; DB 2; Length 71;
Best Local Similarity 50.0%; Pred. No. 2.1;
Matches 36; Conservative 4; Mismatches 27; Indels 5; Gaps 3;

QY 1 AKYAKKEKAYAKKA--EKAA-KKAAKAYKAAEAKKAKAAKAYKAAKAAKAEKAYAAA 57
   ||| :||| ||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2 AKASAAPKKAVAKKAAAPKKAAPKKAAPKKAAPKKAAPKKAAPKKAAPKKAAPKKAAPK 59
   : ||| |||||

QY 58 EAKYKAAKAAKKA 69
   : ||| |||||
Db 60 KVAGKKAARKKA 71

RESULT 10
Q9NF68 ID Q9NF68 PRELIMINARY; PRT; 85 AA.
AC Q9NF68;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Histone H1.
OS Trypanosoma brucei brucei;
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=31285;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=STIB 755, and 1257;
RA Grueter E.;
RL Thesis (2000), Department of Parasitology, Institute of Zoology,
RL SWITZERLAND.
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=STIB 755, and 1257;
RA Grueter E.; Betschart B.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ287591; CAB76173.1; -.
DR EMBL; AJ272459; CAB76169.1; -.
SQ SEQUENCE 85 AA; 8647 MW; CEEFA3AB5269465E CRC64;

Query Match 24.4%; Score 100; DB 2; Length 85;
Best Local Similarity 48.1%; Pred. No. 2.7;
Matches 39; Conservative 3; Mismatches 31; Indels 8; Gaps 4;

QY 2 KKYAKKEKAYAKKAAKAAKAYKAAEAKKAAKAAKAYKAAKAAKAEKAYAAEAKY 61
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 13 KKVAAK-KAVAKKA--APKKAVAK--KAAPKKAVAKKAAAPKKAAPKKAAPKKAAPKKA 67
QY 62 KAAEAAKAYKAAEAAKAAKAAKEA 82
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 68 KKVAPK---KVAGKKAARKKA 85

RESULT 11
Q9NFF2 ID Q9NFF2 PRELIMINARY; PRT; 76 AA.
AC Q9NFF2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Histone H1.
GN Name=H1H76;
OS Trypanosoma brucei brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5702;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=TREU 927/4;
RA Grueter E.;
RL Thesis (2000), Department of Parasitology, Institute of Zoology,
RL SWITZERLAND.
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=TREU 927/4;
RA Grueter E.; Betschart B.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ400880; CAB90836.1; -.
SQ SEQUENCE 76 AA; 7631 MW; 2493E88448B3E0FD CRC64;

Query Match 23.8%; Score 97.5; DB 2; Length 76;
Best Local Similarity 48.1%; Pred. No. 3.6;
Matches 39; Conservative 4; Mismatches 29; Indels 9; Gaps 4;

QY 1 AKYAKKEKAYAKKA--EKAA-KKAAKAYKAAEAKKAAKAAKAYKAAKAAKAEKAYAAA 57
   ||| :||| ||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2 AKTTAAPKKAAPKKAAPKKAAPKKAAPKKAAPKKAAPKKAAPKKAAPKKAAPKKAAPK 59
   : ||| |||||

QY 58 EAKYKAAEAAKAYKAAKAAKAA 78
   : ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 60 KVAPKKVAGKKA---AAKKA 76

RESULT 12
Q9NFJ6 ID Q9NFJ6 PRELIMINARY; PRT; 76 AA.
AC Q9NFJ6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Histone H1.
GN Name=H1B76;
OS Trypanosoma brucei brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5702;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=TREU 927/4;
RA Grueter E.;
RL Thesis (2000), Department of Parasitology, Institute of Zoology,
RL SWITZERLAND.
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=TREU 927/4;
RA Grueter E.; Betschart B.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ287599; CAB76182.1; -.
SQ SEQUENCE 76 AA; 7587 MW; 2959EF4982B2E0F9 CRC64;

Query Match 23.8%; Score 97.5; DB 2; Length 76;

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2005, 11:16:19 ; Search time 157 Seconds
(without alignments)
211.856 Million cell updates/sec

Title: US-10-792-311-6

Perfect score: 409
Sequence: 1 AKYAKKEKAYAKAEKAAK.....KKAYKAEAKAAKAEKAEYEA 86

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1117955

Minimum DB seq length: 0
Maximum DB seq length: 86

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	409	100.0	86	3	AA82576 Copolymer
2	351.5	85.9	77	3	AA82575 Copolymer
3	268	65.5	66	3	AA82574 Copolymer
4	233	57.0	56	3	AA82573 Copolymer
5	138.5	33.9	80	5	AB971044 Tumour ne
6	126.5	30.9	45	3	AA82572 Copolymer
7	115.5	28.2	79	8	ADK10613 Structura
8	115.5	28.2	79	8	ADK15632 Nucleatin
9	115.5	28.2	86	7	ADK10612 Structura
10	115.5	28.2	86	8	ADK15631 Nucleatin
11	115	28.1	60	5	AB971043 Tumour ne
12	113.5	27.8	85	7	ADK10608 Structura
13	113.5	27.8	85	8	ADK15627 Nucleatin
14	112.5	27.5	86	7	ADK10662 Structura
15	112.5	27.5	86	8	ADK15681 Library f
16	111.5	27.3	83	7	ADK10645 Structura
17	111.5	27.3	83	8	ADK15664 Nucleatin
18	110.5	27.0	85	7	ADK10658 Structura
19	110.5	27.0	85	8	ADK15677 Library f
20	109.5	26.8	83	7	ADK10605 Structura
21	109.5	26.8	83	8	ADK15624 Nucleatin
22	108.5	26.5	79	7	ADK10610 Structura
23	108.5	26.5	79	8	ADK15629 Nucleatin
24	108.5	26.5	80	7	ADK10606 Structura
25	108.5	26.5	80	8	ADK15625 Nucleatin

26	108.5	26.5	85	7	ADK10611 Structura
27	108.5	26.5	85	8	ADK15630 Nucleatin
28	108	26.4	35	3	AA82571 Copolymer
29	105.5	25.8	79	7	ADK10660 Structura
30	105.5	25.8	79	8	ADK15679 Library f
31	105.5	25.8	83	7	ADK10695 Structura
32	105.5	25.8	83	8	ADK15714 Library f
33	105.5	25.8	85	7	ADK10661 Structura
34	105.5	25.8	85	8	ADK15680 Library f
35	104.5	25.6	78	7	ADK10604 Structura
36	104.5	25.6	78	8	ADK15623 Nucleatin
37	102	24.9	75	7	ADK10646 Structura
38	102	24.9	75	8	ADK15665 Nucleatin
39	101.5	24.8	46	2	AAW24449 Nucleic a
40	101.5	24.8	60	8	ADK15680 Sea urchi
41	101.5	24.8	60	8	ADK15345 Yeast zuo
42	101.5	24.8	83	7	ADK10655 Structura
43	101.5	24.8	83	8	ADK15674 Library f
44	100	24.4	46	2	AA828871 High affi
45	99	24.2	78	7	ADK10654 Structura

ALIGNMENTS

RESULT 1

AA82576
ID AA82576 standard; peptide; 86 AA.

AC AA82576;

DT 28-JUL-2000 (first entry)

DE Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:6.

KW Copolymer; molecular weight marker; TV-marker; immune disease;

KW glutaric acetate; autoimmune disease; antiarthritic; neuroprotective;

KW osteopathic; immunosuppressive; antithyroid; antiinflammatory;

KW antidiabetic; thyromimetic; haemostatic; antipeptidic; dermatological;

KW antidiabetic; immunosuppressive; demyelinating disease; osteoarthritis;

KW inflammatory condition; multiple sclerosis; rheumatoid arthritis;

KW Crohn's disease; chronic immune thrombocytopenia purpura; colitis;

KW diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis;

KW Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;

KW pemphigus vulgaris; systemic lupus erythematosus.

OS Unidentified.

FN WO200018794-A1.

PD 06-APR-2000.

PP 24-SEP-1999; 99WO-US022402.

XX 25-SEP-1998; 98US-0101693P.

PA (YEDA) YEDA RES & DEV CO LTD.

PA (TEVA-) TEVA PHARM USA INC.

XX Gad A, Lis D;

XX WPI; 2000-317499/27.

XX Copolymer 1 related polypeptides used as molecular weight markers for
glutaric acetate and for treatment and prevention of immune diseases.

XX Claim 10; Page 14; 72pp; English.

XX AA82571 to AA82577 represent specifically claimed copolymer molecular
weight TV-marker polypeptides from the present invention. The present
invention describes polypeptides (I) for determining the molecular weight
of a copolymer (CP), which has an identified molecular weight and an
amino acid composition corresponding to the copolymer. The polypeptides

PA	(TEVA-) TEVA PHARM USA INC.
XX	Gad A, Lis D;
Pt	WPI; 2000-317499/27.
XX	Copolymer 1 related polypeptides used as molecular weight markers for
PT	glatiramer acetate and for treatment and prevention of immune diseases.
XX	Claim 10; Page 14; 72pp; English.
PS	AAY82571 to AAY82577 represent specifically claimed copolymer molecular
XX	weight TV-marker polypeptides from the present invention. The present
CC	invention describes polypeptides (I) for determining the molecular weight
CC	of a copolymer (CP), which has an identified molecular weight and an
CC	amino acid composition corresponding to the copolymer. The polypeptides
CC	of the invention are used as molecular weight markers for glatiramer
CC	acetate related tetrapolymers. The polypeptides may also be used for
CC	treating and preventing immune diseases in a mammal. Autoimmune diseases
CC	which may be treated include either cell-mediated or antibody-mediated
CC	diseases. Such diseases include arthritic conditions, demyelinating
CC	diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid
CC	arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune
CC	cophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, Crohn's
CC	disease, chronic immune thrombocytopenia purpura, colitis, contact
CC	sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's
CC	syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis,
CC	psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-
CC	mediated diseases which can be treated include host-versus-graft disease,
CC	graft-versus-host disease, and delayed-type hypersensitivity. The
CC	polypeptides of the invention have defined molecular weights and physical
CC	properties which are analogous to glatiramer acetate molecules, which
CC	makes them ideal for use as molecular weight markers
XX	
SQ	Sequence 66 AA;
	Query Match 65.5%; Score 368; DB 3; Length 66;
	Best Local Similarity 75.6%; Pred. No. 3e-17;
	Matches 65; Conservative 0; Mismatches 1; Indels 20; Gaps 3
Qy	1 AKYAKKKNVAKAEAKKAAYKAAEAKKYKAAEAKKKAKAAYKAKAKAEKKEYYAAAEAK 60
Dd	1 AKKYAKKCKAVAK-----AKKAEAK-----AAKKAAEKAKKYAKAKAEKKEYYAAAEAK 49
Qy	61 YKAAAKKAYKAAEAANKAAEAAYEEA 86
Dd	50 -----YKAAAKAAKAAEAYEA 66
RESULT 4	
AAY82573	ID AAY82573 standard; peptide; 56 AA.
AC	AC AAY82573;
XX	XX 28-JUL-2000 (first entry)
DE	DE Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:3.
XX	XX Copolymer; molecular weight marker; TV-marker; immune disease;
KW	glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective;
KW	osteopathic; immunosuppressive; antithyroid; antiinflammatory;
KW	antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological;
KW	antianaemic; immunosuppressive; demyelinating disease; osteoarthritis;
KW	inflammatory condition; multiple sclerosis; rheumatoid arthritis;
KW	Crohn's disease; chronic immune thrombocytopenia purpura; colitis;
KW	diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis;
KW	Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
KW	pemphigus vulgaris; systemic lupus erythematosus.
OS	Unidentified.
XX	WO200018794-A1.
PN	XX

[illegible]

PA	(TEVA-) TEVA PHARM USA INC.
XX	Gad A, Lis D;
Pt	WPI; 2000-317499/27.
XX	Copolymer 1 related polypeptides used as molecular weight markers for
PT	glatiramer acetate and for treatment and prevention of immune diseases.
XX	Claim 10; Page 14; 72pp; English.
PS	AAY82571 to AAY82577 represent specifically claimed copolymer molecular
XX	weight TV-marker polypeptides from the present invention. The present
CC	invention describes polypeptides (I) for determining the molecular weight
CC	of a copolymer (CP), which has an identified molecular weight and an
CC	amino acid composition corresponding to the copolymer. The polypeptides
CC	of the invention are used as molecular weight markers for glatiramer
CC	acetate related tetrapolymers. The polypeptides may also be used for
CC	treating and preventing immune diseases in a mammal. Autoimmune diseases
CC	which may be treated include either cell-mediated or antibody-mediated
CC	diseases. Such diseases include arthritic conditions, demyelinating
CC	diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid
CC	arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune
CC	cophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, Crohn's
CC	disease, chronic immune thrombocytopenia purpura, colitis, contact
CC	sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's
CC	syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis,
CC	psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-
CC	mediated diseases which can be treated include host-versus-graft disease,
CC	graft-versus-host disease, and delayed-type hypersensitivity. The
CC	polypeptides of the invention have defined molecular weights and physical
CC	properties which are analogous to glatiramer acetate molecules, which
CC	makes them ideal for use as molecular weight markers
XX	
SQ	Sequence 66 AA;
	Query Match 65.5%; Score 368; DB 3; Length 66;
	Best Local Similarity 75.6%; Pred. No. 3e-17;
	Matches 65; Conservative 0; Mismatches 1; Indels 20; Gaps 3
Qy	1 AKYAKKYNVAKAEAKKAAYKAAEAKKYKAAEAKKKAKAAYKAKAKAEKKEYYAAAEAK 60
Dd	
	1 AKKYAKKCKYAK-----AKKAEAK-----AAKKAAEKAKKYAKAKAEKKEYYAAAEAK 49
Qy	61 YKAAAKKAYKAAEAANKAAEAAYEEA 86
Dd	
	50 -----YKAAAKAAKAAEAYEEA 66
RESULT 4	
ID	AAY82573 standard; peptide; 56 AA.
AC	AAY82573;
XX	
DT	28-JUL-2000 (first entry)
DE	
XX	Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:3.
Kw	Copolymer; molecular weight marker; TV-marker; immune disease;
Kw	glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective;
Kw	osteopathic; immunosuppressive; antithyroid; antiinflammatory;
Kw	antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological;
Kw	antianaemic; immunosuppressive; demyelinating disease; osteoarthritis;
Kw	inflammatory condition; multiple sclerosis; rheumatoid arthritis;
Kw	Crohn's disease; chronic immune thrombocytopenia purpura; colitis;
Kw	diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis;
Kw	Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
Kw	pemphigus vulgaris; systemic lupus erythematosus.
OS	Unidentified.
XX	
PN	WO200018794-A1.


```

XX FH Key Location/Qualifiers
XX FT Misc-difference 9. .16
XX FT /note= "Optionally absent"
XX FT Misc-difference 17. .24
XX FT /note= "Optionally absent"
XX FT Misc-difference 25. .32
XX FT /note= "Optionally absent"
XX FT Misc-difference 33. .40
XX FT /note= "Optionally absent"
XX FT Misc-difference 41. .48
XX FT /note= "Optionally absent"
XX FT Misc-difference 49. .56
XX FT /note= "Optionally absent"
XX FT Misc-difference 57. .64
XX FT /note= "Optionally absent"
XX FT Misc-difference 65. .72
XX FT /note= "Optionally absent"
XX FT Misc-difference 73. .80
XX FT /note= "Optionally absent"
XX PN WO200260488-A1.
XX
XX PD 08-AUG-2002.
XX
XX PF 30-JAN-2002; 2002WO-EP000951.
XX
XX PF 30-JAN-2001; 2001EP-00870017.
XX
XX PR (UYLO-) UNIV CATHOLIQUE LOUVAIN.
XX
XX PI Trouet A, Dubois V;
XX
XX PS WPI; 2002-706887/76.
XX
XX PT New tumor-selective intravascular coagulation inducing molecules useful
XX PT for control of tumor growth.
XX
XX PS Claim 20; Page 27; 40pp; English.
XX
XX CC The invention describes tumour-selective intravascular coagulation
XX CC inducing molecules. The molecules are useful as a medicine and in the
XX CC manufacture of a medicament for the treatment and/or prevention of tumour
XX CC related disorders. The compounds are able to induce blood clotting at
XX CC tumour sites resulting in the disruption of the tumour vascularisation
XX CC and consequently in the control of tumour growth. This sequence
XX CC represents a heparin-binding peptide, a positively charged polymer that
XX CC can be incorporated into a substrate for extracellular hydrolases
XX CC releasable by tumour or neoangiogenic endothelial cells
XX
XX SQ Sequence 80 AA;
XX
XX Query Match 33.9%; Score 138.5; DB 5; Length 80;
XX Best Local Similarity 53.7%; Pred. No. 1.9e-05;
XX Matches 44; Conservative 8; Mismatches 19; Indels 11; Gaps 4;
XX
XX QY 6 KKEKAYAKKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 65
XX DB 4 KAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 56
XX
XX QY 66 A-KKAYKA---EAKAAKAAKAA 83
XX DB 57 ARKKAARKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 78
XX
XX RESULT 6
XX ID AAY82572
XX AC AAY82572;
XX XX 28-JUL-2000 (first entry)
XX

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DE XX Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:2.
XX KW Copolymer; molecular weight marker; TV-marker; immune disease;
XX KW glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective;
XX KW osteopathic; immunosuppressive; antithyroid; antiinflammatory;
XX KW antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological;
XX KW antianemic; immunosuppressive; demyelinating disease; osteoarthritis;
XX KW inflammatory condition; multiple sclerosis; rheumatoid arthritis;
XX KW Crohn's disease; chronic immune thrombocytopaenia purpura; colitis;
XX KW diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis;
XX KW Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
XX KW pemphigus vulgaris; systemic lupus erythematosus.
XX OS Unidentified.
XX XX WO200018794-A1.
XX PN 06-APR-2000.
XX PD 24-SEP-1999; 99WO-US022402.
XX PF 25-SEP-1998; 98US-0101693P.
XX PR (YEDA ) YEDA RES & DEV CO LTD.
XX PA (TEVA-) TEVA PHARM USA INC.
XX PI Gad A, Lis D;
XX XX WPI; 2000-317499/27.
XX
XX PT Copolymer 1 related polypeptides used as molecular weight markers for
XX PT glatiramer acetate and for treatment and prevention of immune diseases.
XX PS Claim 10; Page 14; 72pp; English.
XX
XX CC AAY82571 to AAY82577 represent specifically claimed copolymer molecular
XX CC weight TV-marker polypeptides from the present invention. The present
XX CC invention describes polypeptides (I) for determining the molecular weight
XX CC of a copolymer (CP), which has an identified molecular weight and an
XX CC amino acid composition corresponding to the copolymer. The polypeptides
XX CC of the invention are used as molecular weight markers for glatiramer
XX CC acetate related tetrapolymers. The polypeptides may also be used for
XX CC treating and preventing immune diseases in a mammal. Autoimmune diseases
XX CC which may be treated include either cell-mediated or antibody-mediated
XX CC diseases. Such diseases include arthritic conditions, demyelinating
XX CC diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid
XX CC arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune
XX CC oophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, Crohn's
XX CC disease, chronic immune thrombocytopaenia purpura, colitis, contact
XX CC sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's
XX CC syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis,
XX CC psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-
XX CC mediated diseases which can be treated include host-versus-graft disease,
XX CC graft-versus-host disease, and delayed-type hypersensitivity. The
XX CC polypeptides of the invention have defined molecular weights and physical
XX CC properties which are analogous to glatiramer acetate molecules, which
XX CC makes them ideal for use as molecular weight markers
XX
XX SQ Sequence 45 AA;
XX
XX Query Match 30.9%; Score 126.5; DB 3; Length 45;
XX Best Local Similarity 45.3%; Pred. No. 0.00013;
XX Matches 39; Conservative 0; Mismatches 6; Indels 41; Gaps 3;
XX
XX QY 1 AKKYAKKAYAKKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 60
XX DB 1 AKKYAKK-----AKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 29
XX
XX QY 61 YKAAKAAKAYKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 86
XX DB 30 -----KAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 45
XX

```


RESULT 7
 ID ADEL0613 standard; protein; 79 AA.
 XX AC ADEL0613;
 XX DT 29-JAN-2004 (first entry)
 XX XX Structurally biased random peptide library related protein seqid 20.
 XX XX fusion nucleic acid library; scaffold protein; bioactive peptide;
 KW phenotype change; cell morphology; cell growth; cell viability;
 KW cell adhesion; cellular density; cancer; tumour; apoptosis; cell death;
 KW loss of cell division; decreased cell growth; brca-1; brca-2;
 KW tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC;
 KW Drosophila discs-large; Dlg; cardiovascular; neurobiology; bone biology;
 KW skin biology; cosmetic; endocrinology; infectious disease;
 KW drug toxicity; drug resistance; inflammation; allergic response.
 XX OS Synthetic.
 XX XX US2003143562-A1.
 XX PN 31-JUL-2003.
 XX PD 20-JUN-2002; 2002US-00177725.
 XX PF 08-OCT-1998; 98US-00169015.
 XX PR 08-OCT-1999; 99US-00415765.
 XX XX (RIGE-) RIGEL PHARM INC.
 XX PA Anderson D, Peelle BR, Bogenberger JM;
 XX PI WPI; 2003-829786/77.
 XX DR Novel library of fusion nucleic acids each of which has fused first and
 PT second nucleic acids encoding scaffold protein and library peptide having
 PT alpha helical biasing sequence, respectively, useful in screening
 PT methods.
 XX XX Example 6; SEQ ID NO 20; 110pp; English.
 XX PS The invention describes a library (I) of fusion nucleic acids, where each
 CC fusion nucleic acid comprises a first nucleic acid (N1), encoding a
 CC scaffold protein sequence; and a second nucleic acid (N2), encoding a
 CC library peptide sequence comprising an alpha helical biasing sequence;
 CC where N1 is fused to N2. Disclosed is a method for screening bioactive
 CC peptides conferring a change in specific phenotype such as cell
 CC morphology, cell growth, cell viability, adhesion to substrates or other
 CC cells, and cellular density; changes in the expression of one or more
 CC RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes
 CC in the equilibrium state (i.e., half-life) or one or more RNAs, protein,
 CC lipids, hormones, cytokines, or other molecules; etc. The bioactive
 CC peptide identified by above mentioned method is used to generate more
 CC candidate peptides and to identify target molecules, i.e., the molecules
 CC with which the bioactive peptide interacts. The peptide(s) can be
 CC combined with other pharmacologic activators to study the epistatic
 CC relationships of signal transduction pathways in question. The disclosed
 CC method is also useful in cancer applications. Random libraries can be
 CC introduced into any tumour cell (primary or cultured), and peptides
 CC identified which by themselves induce apoptosis, cell death, loss of cell
 CC division or decreased cell growth. The method is also useful for
 CC screening of bioactive peptides which restore the constitutive function
 CC of the brca-1 or brca-2 genes, and other tumour suppressor genes
 CC important in breast cancer such as the adenomatous polyposis coli gene
 CC (APC) and the Drosophila discs-large gene (Dlg), which are components of
 CC cell-cell junctions. The methods are useful in cardiovascular
 CC applications, neurobiology applications, bone biology applications, skin
 CC biology applications, cosmetic applications, endocrinology
 CC applications, infectious disease applications, drug toxicities and drug
 CC resistance applications, immunobiology, inflammation, and allergic
 CC response applications, and biotechnology applications. The peptide

CC library can easily be monitored, both for its presence within cells and
 CC its quantity. The expression of structurally biased libraries generate
 CC elevated cellular concentration of peptides having a given structural
 CC bias and thus increase the hit rate for targets that bind such
 CC structures. This is the amino acid sequence of a protein associated with
 CC fused nucleic acid and random peptide libraries of the invention.
 XX XX Sequence 79 AA;
 XX Query Match 28.2%; Score 115.5; DB 7; Length 79;
 XX Best Local Similarity 44.2%; Pred. No. 0.0023;
 XX Matches 34; Conservative 16; Mismatches 14; Indels 13; Gaps 3;
 OY 18 AAKAAEAKYKAAEAKKAKAAEAKYKAAEAKK-----EYAAEAKYKAAEAKKA 69
 DB 1 AAEAEAKA-KAAEAEAKAKAQQAQAQAQAQAQAQAQAQAQAQAQAQAQAQAQA 59
 OY 70 YKAAEAKA-AKAAEAKA 82
 DB 60 KEAEAKAEAKAEAKAEAKA 76
 RESULT 8
 ID ADK15632 standard; peptide; 79 AA.
 XX AC ADK15632;
 XX DT 06-MAY-2004 (first entry)
 XX DE Nucleating sequence-containing library fusion protein #14.
 XX XX fusion nucleic acid library; fusion protein library; scaffold protein;
 KW green fluorescent protein; GFP; alpha helical biasing sequence;
 KW nucleating sequence; screening.
 XX OS Synthetic.
 XX XX US2003224412-A1.
 XX PN 04-DEC-2003.
 XX PD 18-MAR-2003; 2003US-00393449.
 XX PF 08-OCT-1998; 98US-00169015.
 XX PR 08-OCT-1999; 99US-00415765.
 XX PR 20-JUN-2002; 2002US-00177725.
 XX XX (ANDE/) ANDERSON D.
 XX PA (PEEL/) PEELLE B R.
 XX PA (BOGE/) BOGENBERGER J M.
 XX PI Anderson D, Peelle BR, Bogenberger JM;
 XX WPI; 2004-033956/03.
 XX DR Library of fusion polypeptides in which each polypeptides comprises
 PT scaffold protein and library peptide having alpha helical biasing
 PT sequence, or scaffold protein, library peptide and nucleating sequence.
 XX XX Example 6; SEQ ID NO 20; 110pp; English.
 XX PS The invention comprises a library of fusion nucleic acids, where each
 CC encoded protein contains a scaffold protein (e.g. a green fluorescent
 CC protein - GFP) and a library peptide sequence comprising an alpha helical
 CC biasing sequence, or a scaffold protein, a library peptide and a
 CC nucleating sequence. The library of the invention is useful for screening
 CC bioactive peptides conferring a particular phenotype. The present amino
 CC acid sequence represents a library protein containing a nucleating
 CC sequence.
 XX XX Sequence 79 AA;

introduced into any tumour cell (primary or cultured), and peptides identified which by themselves induce apoptosis, cell death, loss of cell division or decreased cell growth. The method is also useful for screening of bioactive peptides which restore the constitutive function of the brca-1 or brca-2 genes, and other tumour suppressor genes important in breast cancer such as the adenomatous polyposis coli gene (APC) and the Bcrphilia discs-large gene (Dlg), which are components of cell-cell junctions. The methods are useful in cardiovascular applications, neurobiology applications, bone biology applications, skin biology applications, cosmetic applications, endocrinology applications, infectious disease applications, drug toxicities and drug resistance applications, immunobiology, inflammation, and allergic response applications, and biotechnology applications. The peptide library can easily be monitored, both for its presence within cells and its quantity. The expression of structurally biased libraries generate elevated cellular concentration of peptides having a given structural bias and thus increase the hit rate for targets that bind such structures. This is the amino acid sequence of a protein associated with fused nucleic acid and random peptide libraries of the invention.

Sequence 86 AA;

Query Match 28.2%; Score 115.5; DB 7; Length 86;
Best Local Similarity 39.6%; Pred. No. 0.0025; Indels 2;
Matches 33; Conservative 18; Mismatches 25; Gaps 7;

QY 7 KEKAVAKAEAKKAEEAKA-----YKAAEKKKAKAEAKKYAKAAEKEVEAAAAYK 62
 | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 EEEAKAEAEAKAEAKAEAKKEQQEQKQQEQKQQEQKQQEQKQQEQKQQEQK 60
 | : | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 63 AEAAKVKYKAE-----AKAAAKEA 82
 | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 AKAAEAEEKAKAEAEAKAKAEA 83
 | : | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 10
ADK15631
ID ADK15631 standard; peptide; 86 AA.
XX AC ADK15631;
XX AC
DT 06-MAY-2004 (first entry)
DE XX
XX
XX Nucleating sequence-containing library fusion protein #13.
KW fusion nucleic acid library; fusion protein library; scaffold protein;
KW green fluorescent protein; GFP; alpha helical biasing sequence;
KW nucleating sequence; screening.
OS Synthetic.
OS
PN US2003224412-A1.
XX
PD 04-DEC-2003.
PF 18-MAR-2003; 2003US-00393449.
PF 08-OCT-1998; 98US-00169015.
PR 08-OCT-1999; 99US-00415765.
PR 20-JUN-2002; 2002US-00177725.
PA (ANDE/) ANDERSON D.
PA (PEEL/) PELLIE B R.
PA (BOGE/) BOGENBERGER J M.
XX-Anderson D, Peelle BR, Bogenberger JM;
PI WPI; 2004-033956/03.
DR
XX
XX Library of fusion polypeptides in which each polypeptide comprises
PT scaffold protein and library peptide having alpha helical biasing
PT sequence, or scaffold protein, library peptide and nucleating sequence.
XX

PT methods.

XX PS Example 6; SEQ ID NO 15; 110pp; English.

XX CC The invention describes a library (1) of fusion nucleic acids, where each

CC fusion nucleic acid comprises a first nucleic acid (N1), encoding a

CC scaffold protein sequence; and a second nucleic acid (N2), encoding a

CC library peptide sequence comprising an alpha helical biasing sequence;

CC where N1 is fused to N2. Disclosed is a method for screening bioactive

CC peptides conferring a change in specific phenotype such as cell

CC morphology, cell growth, cell viability, adhesion to substrates or other

CC cells, and cellular density; changes in the expression of one or more

CC RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes

CC in the equilibrium state (i.e., half-life) of one or more RNAs, protein,

CC lipids, hormones, cytokines, or other molecules; etc. The bioactive

CC peptide identified by above mentioned method is used to generate more

CC candidate peptides and to identify target molecules, i.e., the molecules

CC with which the bioactive peptide interacts. The peptide(s) can be

CC combined with other pharmacologic activators to study the epistatic

CC relationships of signal transduction pathways in question. The disclosed

CC method is also useful in cancer applications. Random libraries can be

CC introduced into any tumour cell (primary or cultured), and peptides

CC identified which by themselves induce apoptosis, cell death, loss of cell

CC division or decreased cell growth. The method is also useful for

CC screening of bioactive peptides which restore the constitutive function

CC of the brca-1 or brca-2 genes, and other tumour suppressor genes

CC important in breast cancer such as the adenomatous polyposis coli gene

CC (APC) and the Drosophila discs-large gene (Dlg), which are components of

CC cell-cell junctions. The methods are useful in cardiovascular

CC applications, neurobiology applications, bone biology applications, skin

CC biology applications, cosmetic applications, endocrinology

CC applications, infectious disease applications, drug toxicities and drug

CC resistance applications, immunobiology, inflammation, and allergic

CC response applications, and biotechnology applications. The peptide

CC library can easily be monitored, both for its presence within cells and

CC its quantity. The expression of structurally biased libraries generate

CC elevated cellular concentration of peptides having a given structural

CC bias and thus increase the hit rate for targets that bind such

CC structures. This is the amino acid sequence of a protein associated with

CC fused nucleic acid and random peptide libraries of the invention.

XX SQ Sequence 85 AA;

Query Match 27.8%; Score 113.5; DB 7; Length 85;

Best Local Similarity 41.0%; Pred. No. 0.0038;

Matches 34; Conservative 14; Mismatches 20; Indels 15; Gaps 2;

QY 18 AAKKAEAKAYKAAEAKKKAK-----AEAKKYAKAAKAEKKEAYAAEAAYKA 63

Db 1 AAEAEAKA-KAAAEAKAKEQQKQQKQQKQQKQQKQQKQQKQQKQQKQQKQKEA 59

QY 64 EAAKKAYKAEAKAAKAEAYEA 86

Db 60 KAAAEAKAKAAEAKAEAKAAEA 82

RESULT 13

ADK15627

ID ADK15627 standard; peptide; 85 AA.

XX AC ADK15627;

XX DT 06-MAY-2004 (first entry)

XX DE Nucleating sequence-containing library fusion protein #9.

XX fusion nucleic acid library; fusion protein library; scaffold protein;

KW green fluorescent protein; GFP; alpha helical biasing sequence;

KW nucleating sequence; screening.

XX OS Synthetic.

XX PN US2003224412-A1.

XX PD 04-DEC-2003.

XX PF 18-MAR-2003; 2003US-00393449.

XX PR 08-OCT-1998; 98US-00169015.

XX PR 08-OCT-1999; 99US-00415765.

XX PR 20-JUN-2002; 2002US-00177725.

XX PA (ANDE/) ANDERSON D.

XX PA (PEEL/) PEELLE B R.

XX PA (BOGE/) BOGENBERGER J M.

XX PI Anderson D, Peelle BR, Bogenberger JM;

XX WPI; 2004-033956/03.

XX Library of fusion polypeptides in which each polypeptides comprises

PT scaffold protein and library peptide having alpha helical biasing

PT sequence, or scaffold protein, library peptide and nucleating sequence.

XX Example 6; SEQ ID NO 15; 110pp; English.

XX The invention comprises a library of fusion nucleic acids, where each

CC encoded protein contains a scaffold protein (e.g. a green fluorescent

CC protein - GFP) and a library peptide sequence comprising an alpha helical

CC biasing sequence, or a scaffold protein, a library peptide and a

CC nucleating sequence. The library of the invention is useful for screening

CC bioactive peptides conferring a particular phenotype. The present amino

CC acid sequence represents a library protein containing a nucleating

CC sequence.

XX SQ Sequence 85 AA;

Query Match 27.8%; Score 113.5; DB 8; Length 85;

Best Local Similarity 41.0%; Pred. No. 0.0038;

Matches 34; Conservative 14; Mismatches 20; Indels 15; Gaps 2;

QY 18 AAKKAEAKAYKAAEAKKKAK-----AEAKKYAKAAKAEKKEAYAAEAAYKA 63

Db 1 AAEAEAKA-KAAAEAKAKEQQKQQKQQKQQKQQKQQKQQKQQKQQKQQKQKEA 59

QY 64 EAAKKAYKAEAKAAKAEAYEA 86

Db 60 KAAAEAKAKAAEAKAEAKAAEA 82

RESULT 14

ADE10662

ID ADE10662 standard; protein; 86 AA.

XX AC ADE10662;

XX DT 29-JAN-2004 (first entry)

XX DE Structurally biased random peptide library scaffold protein seqid 69.

XX fusion nucleic acid library; scaffold protein; bioactive peptide;

KW phenotype change; cell morphology; cell growth; cell viability;

KW cell adhesion; cellular density; cancer; tumour; apoptosis; cell death;

KW loss of cell division; decreased cell growth; brca-1; brca-2;

KW tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC;

KW Drosophila discs-large; Dlg; cardiovascular; neurobiology; bone biology;

KW skin biology; cosmetic; endocrinology; infectious disease;

KW drug toxicity; drug resistance; inflammation; allergic response;

KW scaffold protein.

XX OS Synthetic.

XX PN US2003143562-A1.

XX DT 31-JUL-2003.

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Search completed: June 3, 2005, 11:47:09
Job time : 136 secs

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Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	409	100.0	86	4	US-09-405-743A-6	Sequence 6, Appli
2	409	100.0	86	4	US-09-816-989A-6	Sequence 6, Appli
3	351.5	85.9	77	4	US-09-405-743A-5	Sequence 5, Appli
4	351.5	85.9	77	4	US-09-816-989A-5	Sequence 5, Appli
5	268	65.5	66	4	US-09-405-743A-4	Sequence 4, Appli
6	268	65.5	66	4	US-09-816-989A-4	Sequence 4, Appli
7	233	57.0	56	4	US-09-405-743A-3	Sequence 3, Appli
8	233	57.0	56	4	US-09-816-989A-3	Sequence 3, Appli
9	126.5	30.9	45	4	US-09-405-743A-2	Sequence 2, Appli
10	126.5	30.9	45	4	US-09-816-989A-2	Sequence 2, Appli
11	119.5	29.2	35	3	US-08-993-008A-6	Sequence 6, Appli
12	108	26.4	35	3	US-09-405-743A-1	Sequence 1, Appli
13	108	26.4	35	4	US-09-816-989A-1	Sequence 1, Appli
14	106.5	26.0	48	3	US-08-993-008A-5	Sequence 5, Appli
15	101.5	24.8	60	1	US-08-346-849-16	Sequence 16, Appl
16	101.5	24.8	60	2	US-08-293-284A-16	Sequence 16, Appl
17	101.5	24.8	60	4	US-08-898-300-16	Sequence 16, Appl
18	101.5	24.8	60	4	US-08-824-513-16	Sequence 16, Appl
19	93.5	22.9	79	4	US-09-302-540-16642	Sequence 16642, A
20	92	22.5	61	3	US-08-995-172-6	Sequence 6, Appli
21	92	22.5	61	3	US-08-995-172-7	Sequence 7, Appli
22	92	22.5	61	4	US-09-221-050-7	Sequence 7, Appli
23	92	22.5	61	4	US-09-247-054-11	Sequence 11, Appl
24	90	22.0	84	3	US-09-420-592A-8	Sequence 8, Appli
25	90	22.0	84	4	US-09-985-442-8	Sequence 8, Appli
26	90	22.0	84	4	US-09-985-580-8	Sequence 8, Appli
27	89.5	21.9	61	1	US-08-346-849-17	Sequence 17, Appl

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	113.5	21.9	97	2	G60110	repetitive protein
2	101.5	19.6	103	2	S19915	histone H1-like pr
3	94.5	18.2	104	1	H64327	conserved hypothe
4	94	18.1	98	2	H81072	hypothetical prote
5	92.5	17.8	105	1	NSCHH4	nonhistone chrom
6	92	17.7	82	2	T30977	hypothetical prote
7	91.5	17.6	88	2	S02720	outer membrane pr
8	91	17.5	93	2	S04157	outer membrane pr
9	89	17.1	101	2	S65494	sperm-specific pro
10	89	17.1	108	2	B75029	hypothetical prote
11	85.5	16.5	78	2	S06918	DNA-binding protei
12	85.5	16.5	81	2	T26945	hypothetical prote
13	85.5	16.5	107	2	G81080	hypothetical prote
14	83.5	16.1	82	1	QF80	micro glutamic aci
15	83	16.0	108	2	T38936	non-histone chromo
16	81.5	15.7	98	2	S44095	intermediate filam
17	81	15.6	100	2	A33310	nonhistone chrom
18	78.5	15.1	85	1	FDFL4W	antifreeze protein
19	78	15.0	45	2	S04941	protamine phi-3.1
20	78	15.0	92	2	S34115	antifreeze phi-3.1
21	75.5	14.5	97	2	S02376	sperm-specific pro
22	75	14.5	45	2	S10545	antifreeze protein
23	75	14.5	107	1	F69228	protamine phi-3.3
24	74.5	14.4	100	1	NSB0H4	hypothetical prote
25	74	14.3	45	2	S10544	nonhistone chrom
26	74	14.3	69	1	NSPR6	protamine phi-3.2
27	73	14.1	87	2	D81195	nonhistone chrom
28	73	14.1	101	2	S21225	30S ribosomal prot
29	72.5	14.0	106	2	S32032	sperm protein EM6
						Sp17/protein prcu

Qy 94 KAAKAAKAAKAA-AYEA 109
Db 75 EAPAAEAAATEAPAAEA 91

RESULT 5
NSCHH4
nonhistone chromosomal protein HMG-14a - chicken
N;Alternate names: high mobility group protein-14a
C;Species: Gallus gallus (Chicken)
C;Date: 30-Jun-1989 #sequence revision 12-Apr-1996 #text_change 09-Jul-2004
C;Accession: S22122, J0282; J00140
R;Browne, D.L.; Dodgson, J.B.
submitted to the EMBL Data Library, November 1991
A;Description: The chicken HMG-14a gene is transcribed into multiple mRNAs.
A;Reference number: S22122
A;Accession: S22122
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-105 <BRO>
A;Cross-references: UNIPROT:P12902; EMBL:X63086
R;Dodgson, J.B.; Browne, D.L.; Black, A.J.
Gene 63, 287-295, 1988
A;Title: Chicken chromosomal protein HMG-14 and HMG-17 cDNA clones: isolation
A;Reference number: J0283; MUID:88255874; PMID:3384337
A;Accession: J0282
A;Molecule type: mRNA
A;Residues: 2-105 <DOD>
A;Cross-references: GB:M26675; MID:g211920; PIDN:AAA48815.1; PID:g211921
R;Browne, D.L.; Dodgson, J.B.
Gene 124, 199-206, 1993
A;Title: The gene encoding chicken chromosomal protein HMG-14a is transcribed
A;Reference number: J00140; MUID:93185924; PMID:8444343
A;Accession: J00140
A;Molecule type: DNA
A;Residues: 2-5;16-42 <BR2>
A;Cross-references: EMBL:X63083
C;Comment: The HMG proteins are small nonhistone chromosomal proteins, rich
C;Comment: This protein is apparently one of the necessary components of ac
C;Genetics:
A;Gene: HMG-14a
A;Introns: 5/3; 15/3; 25/3; 42/3; 90/3
C;Superfamily: nonhistone chromosomal protein HMG-17
C;Keywords: chromosomal protein; DNA binding; nucleus

Query Match 17.8%; Score 92.5; DB 1; Length 105;
Best Local Similarity 32.0%; Pred. No. 7.8;
Matches 32; Conservative 14; Mismatches 51; Indels 3; Gaps

Qy 1 AKKYAKKAAKAYAKAAKKEKKYAKKAAKAYKAAKKAAYKAAKKAAYKAAKKAAYKAAKKA
Db 8 ARGEAKKEPKRSARLSA---KPAAPPKPEPKKAAAPKKEKAANDKKEDKKAATKGGKGA
Qy 61 YKAAKAYKAAKAAKKEKYAAAEAAKAAKAAKAYKAAEAAKA 100
Db 65 KKGDTKQEDAKEENHSENGTKTNEAPAAEASDDKEAKS 104

RESULT 6
T30977
hypothetical protein C01B10.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30977
R;Blanchard, M.; Bradshaw, H.
submitted to the EMBL Data Library, August 1999
A;Description: The sequence of C. elegans cosmid C01B10..
A;Reference number: Z20949
A;Accession: T30977
A;Status: preliminary; translated from GB/EMBL/DDBY
A;Molecule type: DNA
A;Residues: 1-62 <BLA>

A;Cross-references: UNIPROT:Q17536; EMBL:U58757; PIDN:AAC47916.1

A;Experimental source: strain Bristol N2

C;Genetics:

A;Map position: IV

A;Introns: 27/3; 61/3

A;Note: C01B10.5

Query Match 17.7%; Score 92; DB 2; Length 62;
Best Local Similarity 45.8%; Pred. No. 5.7;
Matches 27; Conservative 4; Mismatches 26; Indels 2; Gaps 1;

Qy 11 AYAKAAKAEKKAYAKAEKAYKAAEA--KKKAKAEAKKYAKAEAKKAEYKAEAKK 67
Db 3 AVQAKVAKTKVAAKPKVKKIQASPKAAAPKAPVKVKAANKSPKAAKPKK 61

RESULT 7

S02720

outer membrane protein H.8 precursor - Neisseria gonorrhoeae

C;Species: Neisseria gonorrhoeae

C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 09-Jul-2004

C;Accession: S02720

R;Woods, J.P.; Spinola, S.M.; Strobel, S.M.; Cannon, J.G.

Mol. Microbiol. 3: 43-48, 1989

A;Title: Conserved lipoprotein H.8 of pathogenic Neisseria consists entirely of pentapep

A;Reference number: S02720; MUID:89237899; PMID:2497298

A;Accession: S02720

A;Molecule type: DNA

A;Residues: 1-88 <W0>

A;Cross-references: UNIPROT:P11910; EMBL:X12627; NID:g44863; PIDN:CAA31145.1; PID:g44864

C;Keywords: membrane protein

F;1-17/Domain: signal sequence #status predicted <SIG>

F;18-88/Product: outer membrane protein H.8 #status predicted <MAT>

Query Match 17.6%; Score 91.5; DB 2; Length 88;
Best Local Similarity 43.0%; Pred. No. 7.9;
Matches 40; Conservative 9; Mismatches 37; Indels 7; Gaps 4;

Qy 14 KKAKEKAEKKAYAKAEKAYKAAEAKKAKAEAKKAYAKAEAKKAYAKAEAKK 73
Db 2 KKSIFAAALLSLALACGGEKAEAA--PAEAS--STEAAPAEAPAEAPAE 55

Qy 74 AEKKEKAEKAEKAEKAEKAYKAEAKKAAKAAKAA 106

Db 56 APAEAPAEAPAEAPAEAA-ATEAPAEAPAEAA 87

RESULT 8

S04157

outer membrane protein H.8 precursor - Neisseria gonorrhoeae

C;Species: Neisseria gonorrhoeae

C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004

C;Accession: S04157

R;Baehr, W.; Gotschlich, E.C.; Hitchcock, P.J.

Mol. Microbiol. 3: 49-55, 1989

A;Title: The virulence-associated gonococcal H.8 gene encodes 14 tandemly repeated penta

A;Reference number: S04157; MUID:89237900; PMID:2497299

A;Accession: S04157

A;Status: not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-93 <BAE>

A;Cross-references: UNIPROT:Q06354; GB:X14739; NID:g288430; PIDN:CAA32869.1; PID:g288431

C;Keywords: membrane protein

Query Match 17.5%; Score 91; DB 2; Length 93;
Best Local Similarity 38.7%; Pred. No. 8.9;
Matches 36; Conservative 10; Mismatches 45; Indels 2; Gaps 2;

Qy 14 KKAKEKAEKKAYAKAEKAYKAAEAKKAKAEAKKAYAKAEKAYAKAEK 73
Db 2 KKSIFAAALLSLALACGGEKAEAPAEASSTEAAPAEAPAEAPAE 60

Qy 74 AEKKEKAEKAEKAEKAEKAYKAEAKKAAKAAKAA 106

Db 61 AAATEAPAEAAATEAPAA-EAPAEAPAEAA 92

RESULT 9

S65494

sperm-specific protein PL-III - North Pacific mussel

C;Species: Mytilus trossulus (North Pacific mussel)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C;Accession: S65494

R;Rocchini, C.; Rice, P.; Ausio, J.

FEBS Lett. 363: 37-40, 1995

A;Title: Complete sequence and characterization of the major sperm nuclear basic protein

A;Reference number: S65494; MUID:95246879; PMID:7729549

A;Accession: S65494

A;Molecule type: protein

A;Residues: 1-101 <ROC>

A;Cross-references: UNIPROT:Q9TXE3; PIDN:AAB34147.1; PID:g998687

C;Keywords: chromosomal protein; DNA binding; nucleosome; sperm

Query Match 17.1%; Score 89; DB 2; Length 101;
Best Local Similarity 25.0%; Pred. No. 13;
Matches 26; Conservative 27; Mismatches 43; Indels 8; Gaps 3;

Qy 2 KKYAKAEKAYAKAEKAYAKAEKAYKAAEAKKAKAEAKKAYAKAEAKK 61
Db 5 RRSKRSRSRSASASPGK---AAKRAKSTPRKGGKARSPSKARRRSRTKTA- 60

Qy 62 KAAKAYAKAAEKKEKYAAAEAKKA-EAAKAYKAEAKKAAAKE 104

Db 61 ---AKRKRSSSPKRRSAGRRVRKGGNRRKSRGKKAANK 101

RESULT 10

B75029

hypothetical protein PAB1179 - Pyrococcus abyssi (strain Orsay)

C;Species: Pyrococcus abyssi

C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004

C;Accession: B75029

R;anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc

A;Reference number: A75001

A;Accession: B75029

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-108 <KAW>

A;Cross-references: UNIPROT:Q9UXU1; GB:AJ248288; GB:AL096836; NID:g5458960; PIDN:CAB5067;

A;Experimental source: strain Orsay

C;Genetics:

C;Gene: PAB1179

C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0223

Query Match 17.1%; Score 89; DB 2; Length 108;
Best Local Similarity 34.1%; Pred. No. 13;
Matches 31; Conservative 15; Mismatches 27; Indels 18; Gaps 3;

Qy 14 KKAKEKAEKKAYAKAEKAY--KAAEAKKAKAEAKKAYAKEA----KAKKEAYKAEAKK 67
Db 13 KAERDAERIERAKEAKAIIRKAREARKIEETLKAEAEAKQLIESKKKEGEAAKR 72

Qy 68 -----YAKAAKAEKKYAAAEAKK 86

Db 73 IMSGEAEISEILSKARDSEKFEKAVSECLK 103

RESULT 11

S06918

DNA-binding protein phi-0 - sea cucumber (Holothuria tubulosa)

C;Species: Holothuria tubulosa

C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004

C;Accession: S06918

R;Prats, E.; Cornudella, L.; Ruiz-Carrillo, A.

Query Match 16.0%; Score 83; DB 2; Length 108;
Best Local Similarity 27.1%; Pred. No. 32;
Matches 29; Conservative 22; Mismatches 38; Indels 18; Gaps 4;
Qy 14 KQAKAAKQKAYAKK---EAKYKAAEAKKAKAE-----AKKYAKEAAKAK 57
Db 3 RAAKSSRRKDPNTPKRNMSAFMPFSIENREKMTDNPDPATFGQLGSLGKRW-KELTSTE 61
Qy 58 KEAYKAAKQKAYKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAKE 104
Db 62 REPVEKARQDKERYERKEYDTKLANGEKTKGA-SAPAAAAAAKE 107

Search completed: June 3, 2005, 11:53:36
Job time : 40 secs

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Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	152	29.3	105	2	Q6N503		Q6N503 rhodospseudo
2	138.5	26.7	98	2	Q8WQ44		Q8WQ44 leishmania
3	127.5	24.6	104	2	Q89JH2		Q89JH2 bradyrhizob
4	126	24.3	94	2	Q7SD04		Q7SD04 neurospora
5	120	23.1	96	2	Q9BNY8		Q9BNY8 leishmania
6	119	22.9	105	2	Q25305		Q25305 leishmania
7	118	22.7	105	2	Q9TVI8		Q9TVI8 leishmania
8	113.5	21.9	97	2	Q7M3W1		Q7M3W1 trypanosoma
9	113	21.8	91	2	Q9NFJ9		Q9NFJ9 trypanosoma
10	112	21.6	104	2	Q7ZJ66		Q7ZJ66 thermus the
11	110	21.2	90	1	H162 TRYCR		Q40274 trypanosoma
12	109.5	21.1	82	2	Q87W81		Q87W81 pseudomonas
13	109	21.0	81	2	Q9N6L9		Q9N6L9 trypanosoma
14	108.5	20.9	68	2	Q26907		Q26907 trypanosoma
15	108	20.8	81	2	Q9NFP6		Q9NFP6 trypanosoma
16	108	20.8	85	2	Q26777		Q26777 trypanosoma
17	108	20.8	92	2	Q9DF23		Q9DF23 myoxocephal
18	107	20.6	76	2	Q9N6J8		Q9N6J8 trypanosoma
19	106	20.4	85	2	Q9N668		Q9N668 trypanosoma
20	105	20.2	76	2	Q9NFI4		Q9NFI4 trypanosoma
21	105	20.2	106	2	Q93WU3		Q93WU3 streptococc
22	105	20.2	106	2	Q93WU7		Q93WU7 streptococc
23	103.5	19.9	101	1	ASR_ENTCFL		Q93Mh6 enterobacte
24	102	19.7	76	2	Q9NGN7		Q9NGN7 trypanosoma
25	102	19.7	76	2	Q9NFJ6		Q9NFJ6 trypanosoma
26	102	19.7	87	1	H1C5 TRYCR		P40269 trypanosoma
27	101.5	19.6	83	2	Q95UN6		Q95UN6 trypanosoma
28	101	19.5	60	2	Q9U3W3		Q9U3W3 caenorhabdi
29	101	19.5	76	2	Q9NG10		Q9NG10 trypanosoma
30	101	19.5	76	2	Q9NFF1		Q9NFF1 trypanosoma
31	101	19.5	76	2	Q9NFF2		Q9NFF2 trypanosoma


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[2]
RN RP SEQUENCE FROM N.A.
RC STRAIN=Friedlin;
RX RMEDLINE=97237563; PubMed=9084041; DOI=10.1016/S0166-6851(96)02801-0;
RA Noll T., Desponds C., Jacquet R., Belli S., Fasel N.J.;
RT "T. Noll, C. Desponds, R. Jacquet, S. Belli and N. J. Fasel. Histone
RL HI expression varies during Leishmania major development.";
RMol. Biochem. Parasitol. 84:215-227(1997).
[3]
RN RP SEQUENCE FROM N.A.
RC STRAIN=Friedlin;
RA Fasel N.J.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ223861; CAA11592.1; -.
DR EMBL; AJ223860; CAA11591.1; -.
SQ SEQUENCE 105 AA; 10819 MW; D9729835131BCE38 CRC64;

Query Match 22.7%; Score 118; DB 2; Length 105;
Best Local Similarity 41.7%; Pred. No. 0.81; Indels 4; Gaps 1;
Matches 35; Conservative 4; Mismatches 41; Indels 4; Gaps 1;

Qy 3 KYAKAEKAYAKAEKAAKAEKAYAKAEKAYAKAEKAAKAEKAYAKAEKAAKAEKAYK 62
Db 26 KRAVGKKTGAKVAKKTGAKVAKKPAKVVKKPAKVVKKPAKVVKKPAKVVKKAVKKA-- 83
Qy 63 AEAKYKAAKAEKKEYYAAAEAKY 86
Db 84 --VKVVVAVKVTAKKSGKSSAKK 105

RESULT 8
Q7M3W1
ID ID Q7M3W1 PRELIMINARY; PRT; 97 AA.
AC AC Q7M3W1;
DT 01-MAR-2004 (T-EMBLrel. 26, Created)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Repetitive protein antigen 69/70 (Fragment).
OS Trypanosoma cruzi.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5693;
RN [1]

SEQUENCE FROM N.A.
RX MEDLINE=89277508; PubMed=2659529;
RA Hofst D.F., Kim K.S., Otsu K.S., Moser D.R., Yost W.J., Blumin J.H.,
RA Donelson J.E., Kirchhoff L.V.;
RT "Trypanosoma cruzi expresses diverse repetitive protein antigens.";
RL Infect. Immun. 57:1959-1967(1989).
DR PIR; G60110;
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR001859; Ribosomal_P2.
DR PRINTS; PR00456; RIBOSOMALP2.
FT NON_TER 1 1
FT NON_TER 97 97
SQ SEQUENCE 97 AA; 8210 MW; 477846BEE0DFE3E2 CRC64;

Query Match 21.9%; Score 113.5; DB 2; Length 97;
Best Local Similarity 47.3%; Pred. No. 1.5;
Matches 43; Conservative 1; Mismatches 42; Indels 5; Gaps 2;

Qy 16 AKAAEKKAYAKAEKAAKAEKAAKAEKAAKAEKAAKAEKAAKAEKAAKAEKAAKAE 75
Db 1 AAAPAKAAAPAKAAAPAKAAAPAKAAAPAKAAAPAKAAAPAKAAAPAKAAAPAKAA 59
Qy 76 KKEYYAAAEKAEKAEKAYKAEKAEKAAKAEKAAKAEKAAKAEKAAKAEKAA 106
Db 60 AKTAAAPAKAAAPAKAAAPAKAAAPAKAAAPAKAAAPAKAAAPAKAAAPAKAA 86

RESULT 9

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QY 72 AKAEKYEYAAAEAKKA-EAAKAYKAEAAKAAKE 104
      | : | | | | | | | | | | | | | |
DB 68 LLARYTERAAEAAKAVREKAMARLLDEAVLVKE 101

RESULT 11
H162_TRYCR STANDARD; PRT; 90 AA.
AC P40274;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Histone H1.M6.2.
OS Trypanosoma cruzi.
OC Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5693;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tulhaden 2;
RX MEDLINE=95059220; PubMed=7969272; DOI=10.1016/0166-6851(94)90082-5;
RA Aaslund L., Carlsson L., Henriksson J., Rydaaker M., Toro G.C.,
RA Galanti N., Petersson U.;
RT "A gene family encoding heterogeneous histone H1 proteins in
      Trypanosoma cruzi.";
RL Mol. Biochem. Parasitol. 65:317-330(1994).
CC -----
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CC or send an email to license@isb-sib.ch)
CC -----
DB EMBL; L27119; AAA66484.1; -.
DR InterPro; IPR005819; Histone H5.
DR PRINTS; PRO0624; HISTONEH5.
DR Chromosomal protein; DNA-binding; Multigene family; Nuclear protein.
KW SEQUENCE 90 AA; 9236 MW; 899950A9D598D6C CRC64;
SQ -----
Query Match 21.2%; Score 110; DB 1; Length 90;
Best Local Similarity 43.9%; Pred. No. 2.3;
Matches 43; Conservative 3; Mismatches 34; Indels 18; Gaps 4;

QY 9 EKAYAKK--AKAAEKKAYKAEKAYKAAEKKAKAEAKKYAEAKKAYKAEAKYKAEAK 66
      : : | | | | | | | | | | | | | | | |
DB 9 KKASPKAAAKKASPKAAAKK-ASPKAAAKTAAKTKAPKAVRKPAKKKA----- 61

QY 67 KYAKAAKAEKGEYAAAEAKKAEAAKAYKAEAAKAAKE 104
      | : | | | | | | | | | | | | | |
DB 62 -----APKKKPA--AKKPAKKAPKAVKKAPKK 90

RESULT 12
Q87W81 PRELIMINARY; PRT; 82 AA.
AC Q87W81;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=PSPTO4673;
OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=323;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DC3000;
RX MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
RA Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,
RA Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
RA Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,

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RA Nelson W.C., Davidsen T.M., Zafar N., Zhou L., Liu J., Yuan Q.,
RA Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,
RA Uterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M.,
RA Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K.,
RA Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,
RA Bender C.L., White O., Fraser C.M., Collmer A.,
RA "The complete genome sequence of the Axibidopsis and tomato pathogen
RT Pseudomonas syringae pv. tomato DC3000.";
DR Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
DR EMBL; AE016872; AA058119.1; -.
DR TIGR; PSPT04673; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 82 AA; 8888 MW; 3826079B39FAD75C CRC64;

Query Match 21.1%; Score 109.5; DB 2; Length 82;
Best Local Similarity 39.0%; Pred. No. 2.3;
Matches 32; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

Qy 5 AKKAEKAYAKKAAKAEKAYAKKAEKAYAKKAEKAYAKKAEKAYAKKAEKAYAKKAE 64
Db 2 AKDKKSGKASKDKL--DKKSPAKSGEAASTLSKSEKKDKKDAEPKKAAD 59
Qy 65 AKYAKAAKAEKAYAAAEAKK 86
Db 60 SKP-EKAKSDKSEKSPAKK 80

RESULT 13
Q9N6L9 PRELIMINARY; PRT; 81 AA.
AC Q9N6L9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Histone H1.
GN Name=H1C81; Synonym=HLB81;
OS Trypanosoma brucei gambiense.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OC NCBI_TaxID=31285;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=STIB 755, and 1257;
RA Grueter E.;
RL Thesis (2000), Department of Parasitology, Institute of Zoology,
RL SWITZERLAND.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=STIB 755, and 1257;
RA Grueter E., Betschart B.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ287596; CAB76178.1; -.
DR EMBL; AJ272460; CAB76170.1; -.
DR GO; GO:0000786; C:nucleosome; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; P:DNA binding; IEA.
DR GO; GO:0006334; P:nucleosome assembly; IEA.
DR InterPro; IPR005819; Histone_H5.
DR PRINTS; PR0624; HISTONEH5.
SQ SEQUENCE 81 AA; 8012 MW; 3610C86DFDED5320 CRC64;

Query Match 21.0%; Score 109; DB 2; Length 81;
Best Local Similarity 50.0%; Pred. No. 2.4;
Matches 44; Conservative 3; Mismatches 29; Indels 12; Gaps 5;

Qy 3 KYAKKAEKAYAKKAAKAEKAYAKKAEKAYAKKAEKAYAKKAEKAYAKKAEKAE 60
Db 3 KASAPKVAKK--AAPKVAKKAP--KKAVAKAPKVAKKAAAPKVAKKAA 57
Qy 61 -YKAEAKKAYAKKAEKAYAAAEAKKA 87
Db 58 PKKAAPKKVPKVKAGK---AAAKKA 81

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RESULT 14
Q26907 PRELIMINARY; PRT; 68 AA.
AC Q26907;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cytoplasmic repetitive antigen (CRA) protein (Fragment).
OS Trypanosoma cruzi.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OC NCBI_TaxID=5693;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89364992; PubMed=2475776; DOI=10.1016/0166-6851(89)90115-1;
RA Lafaille J.J., Linss J., Krieger M.A., Souto-Padron T., de Souza W.,
RA Goldenberg S.;
RT "Structure and expression of two Trypanosoma cruzi genes encoding
RT antigenic proteins bearing repetitive epitopes.";
RL Mol. Biochem. Parasitol. 35:127-136(1989).
DR EMBL; J04016; AAA30177.1; -.
DR InterPro; IPR009761; CRA_rpt.
DR Pfam; PF07046; CRA_rpt; 2.
FT NON TER 1 68
FT NON TER 68 68
SQ SEQUENCE 68 AA; 7208 MW; ED6CF031B3DE7D1F CRC64;

Query Match 20.9%; Score 108.5; DB 2; Length 68;
Best Local Similarity 46.6%; Pred. No. 2.3;
Matches 34; Conservative 8; Mismatches 22; Indels 9; Gaps 3;

Qy 29 EAKYKAAAEAKKAEKAYAKKAEKAYAKKAEKAYAKKAEKAYAKKAEKAYAKKAE 88
Db 4 EAEKQRAAEATKVAEAKQK-AAEATKV-AAEAKQRAAEATKVAEAKQ-----KAAE 54
Qy 89 AAKYKAAEAAKAA 101
Db 55 ATKVAEAKQKAA 67

RESULT 15
Q9NFP6 PRELIMINARY; PRT; 81 AA.
AC Q9NFP6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Histone H1.
GN Name=H1A81;
OS Trypanosoma brucei gambiense.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OC NCBI_TaxID=31285;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1257;
RA Grueter E.;
RL Thesis (2000), Department of Parasitology, Institute of Zoology,
RL SWITZERLAND.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=1257;
RA Grueter E., Betschart B.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ272461; CAB76171.1; -.
DR GO; GO:0000786; C:nucleosome; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; P:DNA binding; IEA.
DR GO; GO:0006334; P:nucleosome assembly; IEA.
DR InterPro; IPR005819; Histone_H5.
DR PRINTS; PR0624; HISTONEH5.
SQ SEQUENCE 81 AA; 8040 MW; 360FC77DE2E24320 CRC64;

Query Match 20.8%; Score 108; DB 2; Length 81;
Best Local Similarity 50.0%; Pred. No. 2.6;

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Matches	47;	Conservative	2;	Mismatches	27;	Indels	18;	Gaps	6;
Qy	15	KAKAAKCKKAYAKKEAKAYKAAEAKKKA--KAEAKKYAKEAAKAKKEA-YKAEAKKYAKA	71						
Db	3	KASAA-PPKAVAKKVAP--KKAVAKKAAAPKKAVAKKAAAPKKAVAKKAAAPK	59						
Qy	72	AKAEKKYAAAEEAKKAEAAKAYKAEAAKAAKAA	105						
Db	60	KAAPKK-----VAPKKVAGK-----KAAAKKA	81						

Search completed: June 3, 2005, 11:52:52
Job time : 172 secs

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OM protein - protein search, using sw model

Run on: June 3, 2005, 11:35:01 ; Search time 158 Seconds
(without alignments)
266.816 Million cell updates/sec

Title: US-10-792-311-7

Perfect score: 519

Sequence: 1 AKYAKAEKAYAKAKAAK.....AKYAKAEKAAKAEKAAVEA 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1202928

Minimum DB seq length: 0
Maximum DB seq length: 109

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	519	100.0	109	3	AAy82577 Copolymer
2	312.5	60.2	86	3	AAy82576 Copolymer
3	289	55.7	77	3	AAy82575 Copolymer
4	228.5	44.0	66	3	AAy82574 Copolymer
5	187	36.0	106	2	Aar06446 Recombina
6	180.5	34.8	56	3	AAy82573 Copolymer
7	179.5	34.6	100	3	AAy8499 Peptide #
8	179.5	34.6	100	3	AAy59044 Amino aci
9	179.5	34.6	100	4	AAy45852 Nucleic a
10	179.5	34.6	100	4	AAU04289 Poly-Lys-
11	146.5	28.2	80	5	Abg71044 Tumour ne
12	141	27.2	100	3	AAy98497 Peptide #
13	141	27.2	100	3	AAy59042 Amino aci
14	141	27.2	100	4	AAy45850 Nucleic a
15	141	27.2	100	4	AAU04287 Poly-L-Ly
16	138	26.6	45	3	AAy82572 Copolymer
17	134.5	25.9	105	7	Adel10636 Copolymer
18	134.5	25.9	105	8	Adel15655 Nucleatin
19	134.5	25.9	106	7	Adel10637 Structura
20	134.5	25.9	106	8	Adel15656 Nucleatin
21	133.5	25.7	104	7	Adel10633 Structura
22	133.5	25.7	104	8	Adel15652 Nucleatin
23	129.5	25.0	106	7	Adel10638 Structura
24	129.5	25.0	106	8	Adel15657 Nucleatin
25	129	24.9	86	7	Adel10612 Structura

26	129	24.9	86	8	ADK15631	Adk15631 Nucleatin
27	128.5	24.8	104	7	ADE10634	Adel10634 Structura
28	128.5	24.8	104	8	ADK15653	Adk15653 Nucleatin
29	128	24.7	83	7	ADE10605	Adel10605 Structura
30	128	24.7	83	8	ADK15624	Adk15624 Nucleatin
31	128	24.7	85	7	ADE10608	Adel10608 Structura
32	128	24.7	85	8	ADK15627	Adk15627 Nucleatin
33	127.5	24.6	104	7	ADE10632	Adel10632 Structura
34	127.5	24.6	104	8	ADK15651	Adk15651 Nucleatin
35	126.5	24.4	104	7	ADE10635	Adel10635 Structura
36	126.5	24.4	104	8	ADK15654	Adk15654 Nucleatin
37	126	24.3	79	7	ADE10609	Adel10609 Structura
38	126	24.3	79	8	ADK15628	Adk15628 Nucleatin
39	125	24.1	79	7	ADE10613	Adel10613 Structura
40	125	24.1	79	8	ADK15632	Adk15632 Nucleatin
41	125	24.1	104	7	ADE10640	Adel10640 Structura
42	125	24.1	104	8	ADK15659	Adk15659 Nucleatin
43	125	24.1	106	7	ADE10639	Adel10639 Structura
44	125	24.1	106	8	ADK15658	Adk15658 Nucleatin
45	122.5	23.6	104	7	ADE10630	Adel10630 Structura

ALIGNMENTS

RESULT 1
AAy82577

XX AAY82577 standard; peptide; 109 AA.

AC AAY82577;

XX 28-JUN-2000 (first entry)

DE DE Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:7.

KW Copolymer; molecular weight marker; TV-marker; immune disease;
KW Glutramer acetate; autoimmune disease; antiarthritic; neuroprotective;
KW osteopathic; immunosuppressive; antithyroid; antiinflammatory;
KW antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological;
KW antianemic; immunosuppressive; demyelinating disease; osteoarthritis;
KW inflammatory condition; multiple sclerosis; rheumatoid arthritis;
KW Crohn's disease; chronic immune thrombocytopenia purpura; colitis;
KW diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis;
KW Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
KW pemphigus vulgaris; systemic lupus erythematosus.

OS Unidentified.

XX WO200018794-A1.

XX 06-APR-2000.

XX 24-SEP-1999; 99WO-US022402.

XX 25-SEP-1998; 98US-0101693P.

XX (YEDA) YEDA RES & DEV CO LTD.
(TEVA-) TEVA PHARM USA-INC.

XX Gad A, Lis D;

XX WPI; 2000-317499/27.

PT Copolymer 1 related polypeptides used as molecular weight markers for
XX glutramer acetate and for treatment and prevention of immune diseases.

PS Claim 10; Page 14; 72pp; English.

XX AAY82571 to AAY82577 represent specifically claimed copolymer molecular
CC weight TV-marker polypeptides from the present invention. The present
CC invention describes polypeptides (I) for determining the molecular weight
CC of a copolymer (CP), which has an identified molecular weight and an
CC amino acid composition corresponding to the copolymer. The polypeptides

AA (YEDA) YEDA .RES & DEV CO LTD.
PA

Copolymer 1 related polypeptides used as molecular weight markers for
PT
glutaram acetate and for treatment and prevention of immune diseases.

[illegible]

KW carcinogenesis; cardiovascular disease; infection.
 XX Synthetic.
 OS US6033884-A.
 PN 07-MAR-2000.
 XX 14-DEC-1993; 93US-00167641.
 XX 20-MAR-1992; 92US-00855389.
 PR 19-MAR-1993; 93WO-US002725.
 XX (BAYU) BAYLOR COLLEGE MEDICINE.
 PA Gottchalk S, Sparrow J, Cristiano RJ, Woo SLC, Smith LC;
 PI WPI; 2000-281993/24.
 DR
 XX
 PT System for transporting nucleic acid into cells, useful e.g. in gene
 therapy and for generating transgenic animals, comprises binding agent
 linked to nucleic acid, surface ligand and lytic agent.
 PT
 XX
 PS Disclosure; Col 125-128; 108pp; English.
 XX

CC The present invention relates to a transporter system for delivering
 CC nucleic acid to a cell. The system comprises a nucleic acid binding
 CC complex, consisting of a binding molecule bonded non-covalently to the
 CC nucleic acid, and covalently to a surface ligand, and a lytic agent. The
 CC binding molecule is spermine or a spermidine derivative. Nucleotide
 CC sequences AAA3693-A3695 and peptide sequences AY98456-Y9850 are used
 CC in the construction of the transporter system of the invention. The
 CC transporter system is used in gene therapy, particularly to deliver
 CC nucleic acids to hepatocytes, muscle cells or bone forming cells, e.g. for
 CC treating cardiovascular disease, cancer, and infection. The transporter
 CC systems are also used to create transgenic animals (as models for human
 CC carcinogenesis or disease or for drug testing). Other uses include
 CC transforming cells to produce proteins, or transfecting cells in vitro
 CC to study the function of the nucleic acid. The use of a surface ligand
 CC allows specific targeting of selected cells and tissues. The lytic agent
 CC provides for release of the nucleic acid into the cellular interior, from
 CC endosomes, without requiring endosomal or lysosomal degradation
 XX
 SQ Sequence 100 AA;

Query Match 34.6%; Score 179.5; DB 3; Length 100;
 Best Local Similarity 55.0%; Pred. No. 7.6e-08;
 Matches 55; Conservative 8; Mismatches 34; Indels 3; Gaps 3;
 Qy 6 KKAEEKAYAK-KAKAAEKKAYAKKAAEKKAAEKKAAEKKAAEKKAAEKKAAEKKAAE 64
 Db 1 KAK 59
 Qy 65 AKKYAKA-AKAAEKKYAAAEKKAAEKKAAEKKAAEKKAAEKKAAEKKAAEKKAAE 103
 Db 60 AK 99

RESULT 8
 ID AAY59044 standard; peptide; 100 AA.
 XX
 AC AAY59044;
 XX
 DT 07-MAR-2000 (first entry)
 XX

DE Amino acid polymer seq ID NO: 64 of US5994109.
 XX Nucleic acid transport system; NTS; cell surface receptor; cytosol;
 XX nuclear membrane; lysis moiety; transgenic animal; human disease;
 KW nucleic acid delivery; cancer.
 XX
 OS Synthetic.

XX Key Location/Qualifiers
 FT Misc-difference 3.100
 FT /note= "Lys-Ala in positions 3 to 100 may be optionally
 FT absent"
 XX
 PN US5994109-A.
 XX 30-NOV-1999.
 XX 03-JUN-1995; 95US-00460890.
 XX 20-MAR-1992; 92US-00855389.
 PR 19-MAR-1993; 93WO-US002725.
 PR 14-DEC-1993; 93US-00167641.
 XX (BAYU) BAYLOR COLLEGE MEDICINE.
 PA Woo SLC, Cristiano RJ, Gottchalk S, Sparrow J, Smith LC;
 PI WPI; 2000-038262/03.
 XX

CC Nucleic acid transport system, useful for creating transgenic animals for
 CC assessing human disease such as cancer in an animal model.
 PT
 XX Disclosure; Col 123-124; 107pp; English.
 XX

CC The invention relates to a nucleic acid transport system (NTS) for
 CC delivering nucleic acid into a cell. The NTS contains but is not limited
 CC to 5 components: (a) the nucleic acid or a macromolecule to be delivered;
 CC (b) a moiety that recognizes and binds to a cell surface receptor or
 CC antigen or is capable of entering a cell through cytosol; (c) a nucleic
 CC acid or macromolecular molecule binding moiety; (d) a moiety that is
 CC capable of moving or initiating movement through a nuclear membrane; and/
 CC or (e) a lysis moiety that enables the transport of the entire complex
 CC from the cell surface directly into the cytoplasm of the cell. The NTS
 CC delivers nucleic acid into the cellular interior as well as the nucleus
 CC of specific cells. The NTS can be used to treat disorders by targeting
 CC specific nucleic acid accordingly. The NTS can also be used to create
 CC transgenic animals for assessing human disease, such as cancer, in an
 CC animal model. The NTS can be used in vitro with tissue culture cells
 CC which allows the role of various nucleic acids to be studied by targeting
 CC specific expression into specifically targeted tissue culture cells. The
 CC lysis agent within the NTS avoids the problem of endosomal/lysosomal
 CC degradation
 XX
 SQ Sequence 100 AA;

Query Match 34.6%; Score 179.5; DB 3; Length 100;
 Best Local Similarity 55.0%; Pred. No. 7.6e-08;
 Matches 55; Conservative 8; Mismatches 34; Indels 3; Gaps 3;
 Qy 6 KKAEEKAYAK-KAKAAEKKAYAKKAAEKKAAEKKAAEKKAAEKKAAEKKAAEKKAAE 64
 Db 1 KAK 59
 Qy 65 AKKYAKA-AKAAEKKYAAAEKKAAEKKAAEKKAAEKKAAEKKAAEKKAAEKKAAE 103
 Db 60 AK 99

RESULT 9
 ID AAB45852 standard; protein; 100 AA.
 XX
 AC AAB45852;
 XX

DT 21-MAR-2001 (first entry)
 XX Nucleic acid transport system peptide ligand SEQ ID NO 64.
 DE Nucleic acid delivery; nucleic acid transporter system; hormone; enzyme;
 KW growth factor; clotting factor; apolipoprotein; receptor; drug; oncogene;
 XX

XX	Unidentified.
OS	
XX	
PN	US6150168-A.
XX	
PD	21-NOV-2000.
XX	
XX	05-JUN-1995; 95US-00460971.
XX	
XX	20-MAR-1992; 92US-00855389.
PR	19-MAR-1993; 93WO-US002725.
PR	14-DEC-1993; 93US-00167641.
XX	
XX	(BAYU) BAYLOR COLLEGE MEDICINE.
PA	
XX	
PI	Gottchalk S, Sparrow J, Cristiano RJ, Smith LC, Woo SLC;
XX	
DR	WPI; 2001-049093/06.
XX	
PT	Nucleic acid transporter system for delivering nucleic acid into a cell,
PT	useful for delivering proteins and polypeptides to cells, including
PT	growth factors, enzymes, hormones, and tumor suppressors.
XX	
PS	Disclosure; Col 123-124; 105pp; English.
XX	
CC	This invention describes a novel system (I) for delivering a nucleic acid
CC	to a cell, comprising a binding complex comprising a ligand binding
CC	molecule noncovalently bound to a nucleic acid and covalently linked to a
CC	surface ligand, and a second binding complex comprising a second binding
CC	molecule noncovalently bound to a nucleic acid and covalently linked to a
CC	nuclear ligand. The complexes are simultaneously bound to the nucleic
CC	acid. The nucleic acid transporter system can also be used in a method
CC	for the in vivo targeting of the insertion of DNA into a cell. It can
CC	also be used in processes for producing transformed cell lines. The
CC	system can be used to deliver a variety of proteins and polypeptides,
CC	such as hormones, growth factors, enzymes, clotting factors,
CC	apoptosis hormones, receptors, drugs, oncogenes, tumor antigens, tumor
CC	suppressors, viral antigens, parasitic antigens, and bacterial antigens.
CC	The transporter system uses lysis agents to overcome the problems of
CC	endosomal/lysosomal degradation seen with prior art systems
XX	
SQ	Sequence 100 AA;
	Query Match 27.2%; Score 141; DB 4; Length 100;
	Best Local Similarity 37.8%; Pred. No. 0.00012;
	Matches 37; Conservative 13; Mismatches 48; Indels 0; Gaps 0;
QY	2 KKYAKTAETKAYAKAAEKKKYAKKAAEKKAYKAAEAKKKKAAEAKKYAKAAKAKKAY 61
	: : : : : : : : : : : : :
Db	1 KKK 60
QY	62 KAAEKKYAKAAEKKYAAAEAKKAAEAKKAYKAAAK 99
	: : : : : : : : : : : :
Db	61 KKK 98
RESULT 15	
AAU04287	
ID	AAU04287 standard; peptide; 100 AA.
XX	
AC	AAU04287;
XX	
DT	
XX	23-OCT-2001 (first entry)
XX	
DE	Poly-L-lysine used in nucleic acid transporter system.
XX	
KW	Nucleic acid transport; cytosol; ligand; lysis agent; spacer molecule;
KW	gene therapy; hepatocyte; muscle; bone forming cell.
XX	
OS	Synthetic.
XX	
Key	Location/Qualifiers
FH	Misc-difference 3.100

[illegible]

Search completed: June 3, 2005, 11:49:54
Job time : 159 secs

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10

1


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;
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-5

Query Match      55.7%; Score 289; DB 9; Length 77;
Best Local Similarity 67.0%; Pred. No. 6.6e-16;
Matches 73; Conservative 1; Mismatches 3; Indels 32; Gaps 4;

QY 1 AKKYAKAEKAYAKAKAAEKKYAKYAKKEKAYAKYAAEAKKAKAAEKKYAKAEKKYAKAEAAKKEA 60
    ||||| ||||| ||||| :|| ||||| ||||| |||||
Db 1 AKKYAKK-EKAYAKKA-----EKAAKKAEAKAYKAAEAKKKA----- 36

QY 61 YKAEAKKYAKAAEKKYEAABAAEAKKAEAAKAYKAAEAKKAAAEAAEYEA 109
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 37 -KAEKKYAKAAEKKYEAABAAEAK-----YKAEAAKAAAEKAEYEA 77

RESULT 6
US-10-792-311-5
; Sequence 5, Application US/10792311
; Publication No. US20050038233A1
; GENERAL INFORMATION:
; APPLICANT: Lis, Doris
; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
; FILE REFERENCE: 2609/60807-A-PCT-US
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/09/816,989
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/101,693
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22402
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-10-792-311-5

Query Match      55.7%; Score 289; DB 17; Length 77;
Best Local Similarity 67.0%; Pred. No. 6.6e-16;
Matches 73; Conservative 1; Mismatches 3; Indels 32; Gaps 4;

QY 1 AKKYAKAEKAYAKAKAAEKKYAKYAKKEKAYAKYAAEAKKAKAAEKKYAKAEKKYAKAEAAKKEA 60
    ||||| ||||| ||||| :|| ||||| ||||| |||||
Db 1 AKKYAKK-EKAYAKKA-----EKAAKKAEAKAYKAAEAKKKA----- 36

QY 61 YKAEAKKYAKAAEKKYEAABAAEAKKAEAAKAYKAAEAKKAAAEAAEYEA 109
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 37 -KAEKKYAKAAEKKYEAABAAEAK-----YKAEAAKAAAEKAEYEA 77

RESULT 7
US-09-816-989A-4
; Sequence 4, Application US/09816989A
; Patent No. US20020115103A1
; GENERAL INFORMATION:
; APPLICANT: Lis, Doris
; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
; FILE REFERENCE: 2609/60807-A-PCT-US
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US/09/816,989A
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22402
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; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-4

Query Match      44.0%; Score 228.5; DB 9; Length 66;
Best Local Similarity 56.9%; Pred. No. 3.1e-11;
Matches 62; Conservative 0; Mismatches 4; Indels 43; Gaps 4;

QY 1 AKKYAKAEKAYAKAKAAEKKYAKYAKKEKAYAKYAAEAKKAKAAEKKYAKAEKKYAKAEAAKKEA 60
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 AKKYAKK-EKAYAKAKKA-----EKAAKKA----- 25

QY 61 YKAEAKKYAKAAEKKYEAABAAEAKKAEAAKAYKAAEAKKAAAEAAEYEA 109
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 26 -KAEKKYAKAAEKKYEAABAAEAK-----YKAEAAKAAAEKAEYEA 66

RESULT 8
US-10-792-311-4
; Sequence 4, Application US/10792311
; Publication No. US20050038233A1
; GENERAL INFORMATION:
; APPLICANT: Gad, Alexander
; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
; FILE REFERENCE: 2609/60807-A-PCT-US
; CURRENT FILING DATE: US/10/792,311
; CURRENT APPLICATION NUMBER: US/09/816,989
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/101,693
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22402
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-10-792-311-4

Query Match      44.0%; Score 228.5; DB 17; Length 66;
Best Local Similarity 56.9%; Pred. No. 3.1e-11;
Matches 62; Conservative 0; Mismatches 4; Indels 43; Gaps 4;

QY 1 AKKYAKAEKAYAKAKAAEKKYAKYAKKEKAYAKYAAEAKKAKAAEKKYAKAEKKYAKAEAAKKEA 60
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 AKKYAKK-EKAYAKAKKA-----EKAAKKA----- 25

QY 61 YKAEAKKYAKAAEKKYEAABAAEAKKAEAAKAYKAAEAKKAAAEAAEYEA 109
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 26 -KAEKKYAKAAEKKYEAABAAEAK-----YKAEAAKAAAEKAEYEA 66

RESULT 9
US-09-816-989A-3
; Sequence 3, Application US/09816989A
; Patent No. US20020115103A1
; GENERAL INFORMATION:
; APPLICANT: Gad, Alexander
; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
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; TITLE OF INVENTION: AND FOR THERAPEUTIC USE
; FILE REFERENCE: 2609/60807-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/816,989A
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/101,693
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22402
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-3

Query Match 34.8%; Score 180.5; DB 9; Length 56;
Best Local Similarity 45.9%; Pred. No. 1.5e-07;
Matches 50; Conservative 3; Mismatches 3; Indels 53; Gaps 3;

Qy 1 AKKYAKAEKAYAKKAAAEKKAYAKAEKAYAKAEKAYAKAEKAYAKAEKAYAKAEKAE 60
Db 1 AKKYAKK-EKAYAKKA-----EKAACKAEKAYAKAEKAEKKAEEK----- 39

Qy 61 YKAEAKYAKAAKAEKKEKYEAAAEAKKAEAAKAYKAEAAKAAKAAKAAKAAKAA 109
Db 40 -----YKAEAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 56

RESULT 10
US-10-792-311-3
; Sequence 3, Application US/10792311
; Publication No. US20050038233A1
; GENERAL INFORMATION:
; APPLICANT: Gad, Alexander
; APPLICANT: Lis, Doris
; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
; FILE REFERENCE: 2609/60807-A-PCT-US
; CURRENT APPLICATION NUMBER: US/10/792,311
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/09/816,989
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/101,693
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22402
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-10-792-311-3

Query Match 34.8%; Score 180.5; DB 17; Length 56;
Best Local Similarity 45.9%; Pred. No. 1.5e-07;
Matches 50; Conservative 3; Mismatches 3; Indels 53; Gaps 3;

Qy 1 AKKYAKAEKAYAKKAAAEKKAYAKAEKAYAKAEKAYAKAEKAYAKAEKAYAKAEKAE 60
Db 1 AKKYAKK-EKAYAKKA-----EKAACKAEKAYAKAEKAEKKAEEK----- 39

Qy 61 YKAEAKYAKAAKAEKKEKYEAAAEAKKAEAAKAYKAEAAKAAKAAKAAKAAKAA 109
Db 40 -----YKAEAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 56
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RESULT 11

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US-09-816-989A-2
; Sequence 2, Application US/09816989A
; Patent No. US20020115103A1
; GENERAL INFORMATION:
; APPLICANT: Gad, Alexander
; APPLICANT: Lis, Doris
; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
; FILE REFERENCE: 2609/60807-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/816,989A
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/101,693
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22402
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-2

Query Match 26.6%; Score 138; DB 9; Length 45;
Best Local Similarity 76.6%; Pred. No. 0.00026;
Matches 36; Conservative 0; Mismatches 7; Indels 4; Gaps 2;

Qy 65 AKKYAKAAKAE--KKEYAAAAEKAAKAAKAYKAEAAKAAKAAKAAKAAKAAKAA 109
Db 1 AKKYAKKAAEKAKAYKAAEAKK--AAKYKAAAEKAAKAAKAAKAAKAAKAAKAA 45

RESULT 12
US-10-792-311-2
; Sequence 2, Application US/10792311
; Publication No. US20050038233A1
; GENERAL INFORMATION:
; APPLICANT: Gad, Alexander
; APPLICANT: Lis, Doris
; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
; FILE REFERENCE: 2609/60807-A-PCT-US
; CURRENT APPLICATION NUMBER: US/10/792,311
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/09/816,989
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/101,693
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22402
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-10-792-311-2

Query Match 26.6%; Score 138; DB 17; Length 45;
Best Local Similarity 76.6%; Pred. No. 0.00026;
Matches 36; Conservative 0; Mismatches 7; Indels 4; Gaps 2;

Qy 65 AKKYAKAAKAE--KKEYAAAAEKAAKAAKAYKAEAAKAAKAAKAAKAAKAAKAA 109
Db 1 AKKYAKKAAEKAKAYKAAEAKK--AAKYKAAAEKAAKAAKAAKAAKAAKAAKAA 45

RESULT 13
US-10-177-725-43
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Result No.	Query			DB	ID	Description
	Score	Match	Length			
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2	519	100.0	109	4	US-09-816-989A-7	Sequence 7, Appli
3	312.5	60.2	86	4	US-09-405-743A-6	Sequence 6, Appli
4	312.5	60.2	86	4	US-09-816-989A-6	Sequence 6, Appli
5	289	55.7	77	4	US-09-405-743A-5	Sequence 5, Appli
6	289	55.7	77	4	US-09-816-989A-5	Sequence 5, Appli
7	228.5	44.0	66	4	US-09-405-743A-4	Sequence 4, Appli
8	228.5	44.0	66	4	US-09-816-989A-4	Sequence 4, Appli
9	180.5	34.8	56	4	US-09-405-743A-3	Sequence 3, Appli
10	180.5	34.8	56	4	US-09-816-989A-3	Sequence 3, Appli
11	179.5	34.6	100	2	US-08-460-890A-64	Sequence 64, Appl
12	179.5	34.6	100	3	US-08-167-641C-64	Sequence 64, Appl
13	179.5	34.6	100	3	US-08-460-971A-64	Sequence 64, Appl
14	179.5	34.6	100	3	US-08-462-040-64	Sequence 62, Appl
15	141	27.2	100	2	US-08-460-890A-62	Sequence 62, Appl
16	141	27.2	100	3	US-08-167-641C-62	Sequence 62, Appl
17	141	27.2	100	3	US-08-460-971A-62	Sequence 62, Appl
18	141	27.2	100	3	US-08-462-040-62	Sequence 62, Appl
19	138	26.6	45	4	US-09-405-743A-2	Sequence 2, Appli
20	138	26.6	45	4	US-09-816-989A-2	Sequence 2, Appli
21	126.5	24.4	56	3	US-08-993-008A-6	Sequence 6, Appli
22	122	23.5	88	4	US-09-107-532A-6745	Sequence 6745, Ap
23	119	22.9	96	2	US-08-668-255-7	Sequence 7, Appli
24	118	22.7	105	2	US-08-668-255-5	Sequence 5, Appli
25	115	22.2	102	4	US-09-101-751A-90	Sequence 90, Appl
26	114	22.0	93	4	US-09-107-532A-6743	Sequence 6743, Ap
27	110.5	21.3	48	3	US-08-993-008A-5	Sequence 5, Appli


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; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-7

Query Match          100.0%; Score 519; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 7.7e-37;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKYAKKAEKAYAKKAAKAEKKAYAKKEKAYAKAEKKAAYKAAEKKKAKAEKKYAKAEAAKAKEA 60
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DB 1 AKKYAKKAEKAYAKKAAKAEKKAYAKKEKAYAKAEKKAAYKAAEKKKAKAEKKYAKAEAAKAKEA 60
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QY 61 YKAEAKKYAKAAKAEKKEYAAAEAKKAAEAAKAYKAAEAAKAAAEAAEAAVEA 109
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DB 61 YKAEAKKYAKAAKAEKKEYAAAEAKKAAEAAKAYKAAEAAKAAAEAAEAAVEA 109
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RESULT 3
US-09-405-743A-6
; Sequence 6, Application US/09405743A
; Patent No. 6514938
; GENERAL INFORMATION:
; APPLICANT: Yeda Research and Development Co., Ltd.
; TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
; FILE REFERENCE: 60807-A
; CURRENT APPLICATION NUMBER: US/09/405,743A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PEPTIDE
US-09-405-743A-6

Query Match          60.2%; Score 312.5; DB 4; Length 86;
Best Local Similarity 72.1%; Pred. No. 1.1e-19;
Matches 80; Conservative 1; Mismatches 3; Indels 27; Gaps 5;

QY 1 AKKYAKKAEKAYAKKAAKAEKKAYAKKEKAYAKAEKKAAYKAAEKKKAKAEKKYAKAEAAKAKEA 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 AKKYAKK-EKAYAKKA-----EKAACKAEAKAYKAAEAKKKA----- 36
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 YKAEAKKYAKAAKAEKKEYAAAEAK-KAEAA-KAYKAEAAKAAAEAAVEA 109
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 37 -KAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAYKAEAAKAAAEAAVEA 86
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 4
US-09-816-989A-6
; Sequence 6, Application US/09816989A
; Patent No. 6800287
; GENERAL INFORMATION:
; APPLICANT: Gad, Alexander
; APPLICANT: Lis, Doris
; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
; FILE REFERENCE: 2609/60807-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/816,989A
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/101,693
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22402
; PRIOR FILING DATE: 1999-09-24
```

```
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-6

Query Match          60.2%; Score 312.5; DB 4; Length 86;
Best Local Similarity 72.1%; Pred. No. 1.1e-19;
Matches 80; Conservative 1; Mismatches 3; Indels 27; Gaps 5;

QY 1 AKKYAKKAEKAYAKKAAKAEKKAYAKKEKAYAKAEKKAAYKAAEKKKAKAEKKYAKAEAAKAKEA 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 AKKYAKK-EKAYAKKA-----EKAACKAEAKAYKAAEAKKKA----- 36
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 YKAEAKKYAKAAKAEKKEYAAAEAK-KAEAA-KAYKAEAAKAAAEAAVEA 109
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 37 -KAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAYKAEAAKAAAEAAVEA 86
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 5
US-09-405-743A-5
; Sequence 5, Application US/09405743A
; Patent No. 6514938
; GENERAL INFORMATION:
; APPLICANT: Yeda Research and Development Co., Ltd.
; TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
; FILE REFERENCE: 60807-A
; CURRENT APPLICATION NUMBER: US/09/405,743A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PEPTIDE
US-09-405-743A-5

Query Match          55.7%; Score 289; DB 4; Length 77;
Best Local Similarity 67.0%; Pred. No. 8.8e-18;
Matches 73; Conservative 1; Mismatches 3; Indels 32; Gaps 4;

QY 1 AKKYAKKAEKAYAKKAAKAEKKAYAKKEKAYAKAEKKAAYKAAEKKKAKAEKKYAKAEAAKAKEA 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 AKKYAKK-EKAYAKKA-----EKAACKAEAKAYKAAEAKKKA----- 36
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 YKAEAKKYAKAAKAEKKEYAAAEAK-KAEAA-KAYKAEAAKAAAEAAVEA 109
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 37 -KAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAYKAEAAKAAAEAAVEA 77
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 6
US-09-816-989A-5
; Sequence 5, Application US/09816989A
; Patent No. 6800287
; GENERAL INFORMATION:
; APPLICANT: Gad, Alexander
; APPLICANT: Lis, Doris
; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI
; FILE REFERENCE: 2609/60807-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/816,989A
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/101,693
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22402
; PRIOR FILING DATE: 1999-09-24
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; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-3

Query Match          34.8%; Score 180.5; DB 4; Length 56;
Best Local Similarity 45.9%; Pred. No. 7.4e-09;
Matches 50; Conservative 3; Mismatches 3; Indels 53; Gaps 3;

Qy 1 AKYAKAEKAYAKAKAAKAEKKAYAKAEKAYAKAAEKKAKAEKKYAKAEAAKKEA 60
      ||||| ||||| ||||| :|| | ||||| ||||| ||||| :||
Db 1 AKYAKK-EKAYAKA-----EKAAKAEKAYAKAEKKYAKAEKKYAKAK 39
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 61 YKAEAKYAKAKAEKKEKAYAAAEKAEAAKAYKAEAAKAAAEKAEAYEA 109
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 40 -----YKAEAAKAAAEKAEAYEA 56
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
US-08-460-890A-64
; Sequence 64, Application US/08460890A
; Patent No. 5994109
; GENERAL INFORMATION:
; APPLICANT: Woo, Savio L.C.
; APPLICANT: Smith, Louis C.
; APPLICANT: Cristiano, Richard J.
; APPLICANT: Gottchalk, Stephen
; TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
; TITLE OF INVENTION: METHODS OF USE
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,890A
; FILING DATE: June 5, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/855,389
; FILING DATE: March 19, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/066
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
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```
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be
; OTHER INFORMATION: present or absent.
US-08-460-890A-64

Query Match          34.6%; Score 179.5; DB 2; Length 100;
Best Local Similarity 55.0%; Pred. No. 1.6e-08;
Matches 55; Conservative 8; Mismatches 34; Indels 3; Gaps 3;

Qy 6 KKAEEKYAK-KAKAAEKKEKAYAKKEAKYKAAEAKKKAKAEAKKYAKAEAAKKEAYKAE 64
      ||||| ||||| :|| | ||||| ||||| ||||| :||
Db 1 KAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAK 59
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 65 AKKYAKA-KAAEKKEKAYAAAEKAEAAKAYKAEAAKAAAK 103
      ||||| ||||| :|| | ||||| ||||| ||||| |||||
Db 60 AKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAK 99
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 12
US-08-167-641C-64
; Sequence 64, Application US/08167641C
; Patent No. 6033884
; GENERAL INFORMATION:
; APPLICANT: Woo, Savio L.C.
; APPLICANT: Smith, Louis C.
; APPLICANT: Cristiano, Richard J.
; APPLICANT: Gottchalk, Stephen
; TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
; TITLE OF INVENTION: METHODS OF USE
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/167,641C
; FILING DATE: December 14, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/855,389
; FILING DATE: March 20, 1992
; APPLICATION NUMBER: PCT/US93/02725
; FILING DATE: March 19, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 205/012
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be
; OTHER INFORMATION: present or absent.
```


US-08-167-641C-64

Query Match 34.6%; Score 179.5; DB 3; Length 100;
Best Local Similarity 55.0%; Pred. No. 1.6e-08;
Matches 55; Conservative 8; Mismatches 34; Indels 3; Gaps 3;
Qy 6 KKAEEKAYAK-KAKAAEKKAYAKKAAEAKKAYAKAAEAKKAYAKAAEAKKAYAK 64
Db 1 KAK 59
Qy 65 AKYAKA-AKAEKKEVAAAEAKKAAEAKKAYAKAAEAKKAAK 103
Db 60 AK 99

RESULT 13

US-08-460-971A-64
; Sequence 64, Application US/08460971A
; Patent No. 6150168
; GENERAL INFORMATION:
; APPLICANT: Woo, Savio L.C.
; APPLICANT: Smith, Louis C.
; APPLICANT: Cristiano, Richard J.
; APPLICANT: Gottchalk, Stephen
; TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
; TITLE OF INVENTION: METHODS OF USE
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,971A
; FILING DATE: June 5, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/167,641
; FILING DATE: December 14, 1993
; APPLICATION NUMBER: 07/855,389
; FILING DATE: March 20, 1992
; APPLICATION NUMBER: PCT/US93/02725
; FILING DATE: March 19, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/063
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be
; OTHER INFORMATION: present or absent.
US-08-460-971A-64

Query Match

34.6%; Score 179.5; DB 3; Length 100;

Best Local Similarity 55.0%; Pred. No. 1.6e-08;
Matches 55; Conservative 8; Mismatches 34; Indels 3; Gaps 3;

Qy 6 KKAEEKAYAK-KAKAAEKKAYAKKAAEAKKAYAKAAEAKKAYAKAAEAKKAYAK 64
Db 1 KAK 59
Qy 65 AKYAKA-AKAEKKEVAAAEAKKAAEAKKAYAKAAEAKKAAK 103
Db 60 AK 99

RESULT 14

US-08-462-040-64
; Sequence 64, Application US/08462040
; Patent No. 6177554
; GENERAL INFORMATION:
; APPLICANT: Woo, Savio L.C.
; APPLICANT: Smith, Louis C.
; APPLICANT: Cristiano, Richard J.
; APPLICANT: Gottchalk, Stephen
; TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
; TITLE OF INVENTION: METHODS OF USE
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,040
; FILING DATE: June 5, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/167,641
; FILING DATE: December 14, 1993
; APPLICATION NUMBER: 07/855,389
; FILING DATE: March 20, 1992
; APPLICATION NUMBER: PCT/US93/02725
; FILING DATE: March 19, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be
; OTHER INFORMATION: present or absent.
US-08-462-040-64

Query Match 34.6%; Score 179.5; DB 3; Length 100;
Best Local Similarity 55.0%; Pred. No. 1.6e-08;
Matches 55; Conservative 8; Mismatches 34; Indels 3; Gaps 3;

